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1

SEQUENCE LISTING

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Zelder, Oskar
Kolpprogge, Corinna
Schroder, Hartwig
Hafner, Stefan

<120> Method for Zymotic Production of Fine Chemicals Containing Sulphur (Meta)

<130> 13111-00002-US

<150> PCT/EP 2003/009452

<151> 2003-08-26

<150> DE 102 39 073.8

<151> 2002-08-26

<160> 69

<170> PatentIn version 3.3

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Asp Gly Lys Pro Trp Gly Ser Arg Phe Pro Ala Leu Ser Ile Arg Asp
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Ile Ser Ala Ile Glu Leu Asp Pro His Trp Asn Gly Gly Asp Tyr Tyr
 180 185 190

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His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg Phe Gly Thr
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225

230

235

240

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Asn Arg His Asp Ile Gly Arg Gly Arg Gly Leu Asn Lys Ala Leu
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Thr Arg Asp Asn Val Val Met Val Leu His Ala Leu Thr Gly Asp Ser
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His Ile Thr Gly Pro Ala Gly Pro Gly His Xaa Thr Pro Gly Trp Trp
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Asp Trp Ile Ala Gly Pro Gly Ala Pro Ile Asp Thr Asn Arg Trp Cys
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Ala Ile Ala Thr Asn Val Leu Gly Gly Cys Arg Gly Ser Thr Gly Pro
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Leu Asn Ser His Asp Val Gly Arg Gly Arg Gly Val Ser Ala Ala			
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260 265 270	
ccc agg cag gag cag gag gaa ctt gcc cgcc ctc att ccc ggc tca cgcc Pro Arg Gln Glu Gln Glu Leu Ala Arg Leu Ile Pro Gly Ser Arg	864
275 280 285	
ctg ctt ttc ctt gac gaa ccc tat ggc cac gac gcc ttt ctt atc gac Leu Leu Phe Leu Asp Glu Pro Tyr Gly His Asp Ala Phe Leu Ile Asp	912
290 295 300	
acc gag acc gtc agc cgcc atg gtc tgc gag ttc aag agg cag ttg ata Thr Glu Thr Val Ser Arg Met Val Cys Glu Phe Lys Arg Gln Leu Ile	960
305 310 315 320	
gtt gac aat tga Val Asp Asn	972

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<213> Chlorobium tepidum

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Ser Trp Trp Cys Gly Met Phe Gly Glu Gly Arg Ala Phe Asp Glu Thr	
35 40 45	
Arg Asp Phe Ile Val Cys Ser Asn Val Leu Gly Ser Cys Tyr Gly Thr	
50 55 60	
Thr Gly Pro Met Ser Val Asn Pro Leu Ser Gly Arg His Tyr Gly Pro	
65 70 75 80	
Asp Phe Pro Arg Ile Thr Ile Arg Asp Met Val Asn Val Gln Arg Leu	
85 90 95	
Leu Leu Arg Ser Leu Gly Ile Asp Arg Ile Arg Leu Ile Val Gly Ala	

100	105	110
Ser Leu Gly Gly Met Gln Val Leu Glu Trp Gly Ala Met Tyr Pro Glu		
115	120	125
Met Ala Gly Ala Leu Met Pro Met Gly Val Ser Gly Arg His Ser Ala		
130	135	140
Trp Cys Ile Ala Gln Ser Glu Ala Gln Arg Gln Ala Ile Ala Ala Asp		
145	150	155
Ala Glu Trp Gln Asp Gly Trp Tyr Asp Pro Glu Val Gln Pro Arg Lys		
165	170	175
Gly Leu Ala Ala Ala Arg Met Met Ala Met Cys Thr Tyr Arg Cys Phe		
180	185	190
Glu Asn Tyr Gln Gln Arg Phe Gly Arg Lys Gln Arg Glu Asp Gly Leu		
195	200	205
Phe Glu Ala Glu Ser Tyr Val Arg His Gln Gly Asp Lys Leu Val Gly		
210	215	220
Arg Phe Asp Ala Asn Thr Tyr Ile Thr Leu Thr Arg Ala Met Asp Met		
225	230	235
His Asp Leu Gly Arg Gly Arg Asp Ser Tyr Glu Ala Ala Leu Gly Ala		
245	250	255
Leu Lys Met Pro Val Glu Ile Leu Ser Ile Asp Ser Asp Val Leu Tyr		
260	265	270
Pro Arg Gln Glu Gln Glu Glu Leu Ala Arg Leu Ile Pro Gly Ser Arg		
275	280	285
Leu Leu Phe Leu Asp Glu Pro Tyr Gly His Asp Ala Phe Leu Ile Asp		
290	295	300
Thr Glu Thr Val Ser Arg Met Val Cys Glu Phe Lys Arg Gln Leu Ile		
305	310	315
320		
Val Asp Asn		

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<213> Caulobacter crescentus

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<222> (1)..(1146)
<223> RCO00727

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20 25 30	
ggt ctg gaa atc gcc tac cag acc tac ggc cag ctg aac g ^c gac aag Gly Leu Glu Ile Ala Tyr Gln Thr Tyr Gly Gln Leu Asn Ala Asp Lys	144
35 40 45	
tcc aac gcc gtc ctg atc tgc cac gcc ctg acg ggc gac cag cat gtg Ser Asn Ala Val Leu Ile Cys His Ala Leu Thr Gly Asp Gln His Val	192
50 55 60	
gcc tcg ccc cac ccc acc acc ggc aag ccc ggc tgg tgg caa cgc ctt Ala Ser Pro His Pro Thr Thr Gly Lys Pro Gly Trp Trp Gln Arg Leu	240
65 70 75 80	
gtt ggt ccc ggt aag cc ^g ctg gat ccc g ^c g ^g c ^a ttc atc atc tgc Val Gly Pro Gly Lys Pro Leu Asp Pro Ala Arg His Phe Ile Ile Cys	288
85 90 95	
tcg aac gtg atc ggc ggc tgc atg ggc tcg acg ggc cc ^g gcc tcg atc Ser Asn Val Ile Gly Gly Cys Met Gly Ser Thr Gly Pro Ala Ser Ile	336
100 105 110	
aat cc ^g gcc acg ggc aag acc tat ggc ctg tcg ttc cca gtc atc acc Asn Pro Ala Thr Gly Lys Thr Tyr Gly Leu Ser Phe Pro Val Ile Thr	384
115 120 125	
atc gcc gat atg gtg cg ^g gcc cag gcc atg ctg gtc tct g ^c ctc ggg Ile Ala Asp Met Val Arg Ala Gln Ala Met Leu Val Ser Ala Leu Gly	432
130 135 140	
gtc gag acc ctg ttc gcc gtc ggc ggc tcg atg ggc ggc atg cag Val Glu Thr Leu Phe Ala Val Val Gly Gly Ser Met Gly Gly Met Gln	480
145 150 155 160	
gtc cag caa tgg gcc gtg gac tat ccc gag cg ^g atg ttc agc gcc gtg Val Gln Gln Trp Ala Val Asp Tyr Pro Glu Arg Met Phe Ser Ala Val	528
165 170 175	
gtg ctg gcc tcg gcc tcg cgc cac tcg gcc cag aac atc g ^c g ^g ttc cac Val Leu Ala Ser Ala Ser Arg His Ser Ala Gln Asn Ile Ala Phe His	576
180 185 190	
gag gtg ggc cgc cag g ^c g ^g atc atg gcc gat ccc gac tgg cgc ggc ggc Glu Val Gly Arg Gln Ala Ile Met Ala Asp Pro Asp Trp Arg Gly Gly	624
195 200 205	
gcc tat gcc gag cac ggc gtg cg ^g ccc gag aag ggc ctg gcc gtg g ^c Ala Tyr Ala Glu His Gly Val Arg Pro Glu Lys Gly Leu Ala Val Ala	672
210 215 220	
cg ^g atg gcc g ^c g ^g cac atc acc tat ctg tcc gag ccc gcc ctg cag cg ^g Arg Met Ala Ala His Ile Thr Tyr Leu Ser Glu Pro Ala Leu Gln Arg	720
225 230 235 240	
aag ttc ggc cgc gag cta cag cgc gac ggc ctc tcc tgg ggc ttt gac Lys Phe Gly Arg Glu Leu Gln Arg Asp Gly Leu Ser Trp Gly Phe Asp	768
245 250 255	

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Ala Asp Phe Gln Val Glu Ser Tyr Leu Arg His Gln Gly Ser Ser Phe																																																													
260	265	270		gtc gac cggttc gac gcc aac agc tat ctc tac atc acc cggtcc atg	864	Val Asp Arg Phe Asp Ala Asn Ser Tyr Leu Tyr Ile Thr Arg Ala Met		275	280	285		gac tat ttc gac atc gcc gcc agc cat ggc ggg gtgt ctg gcc aag gcg	912	Asp Tyr Phe Asp Ile Ala Ala Ser His Gly Gly Val Leu Ala Lys Ala		290	295	300		ttc acc cga gcg cggttgc ttc tgc gtgt ctg agc ttc tcc agc	960	Phe Thr Arg Ala Arg Asn Val Arg Phe Cys Val Leu Ser Phe Ser Ser		305	310	315	320	gac tgg ctc tat ccg acc gcc gag aac cgc cac ctg gtc cgccgtc	1008	Asp Trp Leu Tyr Pro Thr Ala Glu Asn Arg His Leu Val Arg Ala Leu		325	330	335		acc gcc gcc ggg gcc cgc gcg gcc ttc gcc gag atc gag agc gac aag	1056	Thr Ala Ala Gly Ala Arg Ala Ala Phe Ala Glu Ile Glu Ser Asp Lys		340	345	350		ggc cat gac gcc ttc ctg ctg gac gag ccg gtgt atg gac gcc gcg ctg	1104	Gly His Asp Ala Phe Leu Leu Asp Glu Pro Val Met Asp Ala Ala Leu		355	360	365		gaa ggc ttc ctg gcc tcg gaa cgc gat ccg ggg ctg gtt	1146	Glu Gly Phe Leu Ala Ser Ala Glu Arg Asp Arg Gly Leu Val		370	375	380		tga	1149
270																																																													
gtc gac cggttc gac gcc aac agc tat ctc tac atc acc cggtcc atg	864																																																												
Val Asp Arg Phe Asp Ala Asn Ser Tyr Leu Tyr Ile Thr Arg Ala Met																																																													
275	280	285		gac tat ttc gac atc gcc gcc agc cat ggc ggg gtgt ctg gcc aag gcg	912	Asp Tyr Phe Asp Ile Ala Ala Ser His Gly Gly Val Leu Ala Lys Ala		290	295	300		ttc acc cga gcg cggttgc ttc tgc gtgt ctg agc ttc tcc agc	960	Phe Thr Arg Ala Arg Asn Val Arg Phe Cys Val Leu Ser Phe Ser Ser		305	310	315	320	gac tgg ctc tat ccg acc gcc gag aac cgc cac ctg gtc cgccgtc	1008	Asp Trp Leu Tyr Pro Thr Ala Glu Asn Arg His Leu Val Arg Ala Leu		325	330	335		acc gcc gcc ggg gcc cgc gcg gcc ttc gcc gag atc gag agc gac aag	1056	Thr Ala Ala Gly Ala Arg Ala Ala Phe Ala Glu Ile Glu Ser Asp Lys		340	345	350		ggc cat gac gcc ttc ctg ctg gac gag ccg gtgt atg gac gcc gcg ctg	1104	Gly His Asp Ala Phe Leu Leu Asp Glu Pro Val Met Asp Ala Ala Leu		355	360	365		gaa ggc ttc ctg gcc tcg gaa cgc gat ccg ggg ctg gtt	1146	Glu Gly Phe Leu Ala Ser Ala Glu Arg Asp Arg Gly Leu Val		370	375	380		tga	1149								
285																																																													
gac tat ttc gac atc gcc gcc agc cat ggc ggg gtgt ctg gcc aag gcg	912																																																												
Asp Tyr Phe Asp Ile Ala Ala Ser His Gly Gly Val Leu Ala Lys Ala																																																													
290	295	300		ttc acc cga gcg cggttgc ttc tgc gtgt ctg agc ttc tcc agc	960	Phe Thr Arg Ala Arg Asn Val Arg Phe Cys Val Leu Ser Phe Ser Ser		305	310	315	320	gac tgg ctc tat ccg acc gcc gag aac cgc cac ctg gtc cgccgtc	1008	Asp Trp Leu Tyr Pro Thr Ala Glu Asn Arg His Leu Val Arg Ala Leu		325	330	335		acc gcc gcc ggg gcc cgc gcg gcc ttc gcc gag atc gag agc gac aag	1056	Thr Ala Ala Gly Ala Arg Ala Ala Phe Ala Glu Ile Glu Ser Asp Lys		340	345	350		ggc cat gac gcc ttc ctg ctg gac gag ccg gtgt atg gac gcc gcg ctg	1104	Gly His Asp Ala Phe Leu Leu Asp Glu Pro Val Met Asp Ala Ala Leu		355	360	365		gaa ggc ttc ctg gcc tcg gaa cgc gat ccg ggg ctg gtt	1146	Glu Gly Phe Leu Ala Ser Ala Glu Arg Asp Arg Gly Leu Val		370	375	380		tga	1149																
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ttc acc cga gcg cggttgc ttc tgc gtgt ctg agc ttc tcc agc	960																																																												
Phe Thr Arg Ala Arg Asn Val Arg Phe Cys Val Leu Ser Phe Ser Ser																																																													
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acc gcc gcc ggg gcc cgc gcg gcc ttc gcc gag atc gag agc gac aag	1056																																																												
Thr Ala Ala Gly Ala Arg Ala Ala Phe Ala Glu Ile Glu Ser Asp Lys																																																													
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gaa ggc ttc ctg gcc tcg gaa cgc gat ccg ggg ctg gtt	1146																																																												
Glu Gly Phe Leu Ala Ser Ala Glu Arg Asp Arg Gly Leu Val																																																													
370	375	380		tga	1149																																																								
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<213> Caulobacter crescentus

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10																																					
15																																					
Phe Pro Ala Asn Glu Pro Leu Arg Leu Asp Ser Gly Gly Val Ile Glu																																					
20	25	30		Gly Leu Glu Ile Ala Tyr Gln Thr Tyr Gly Gln Leu Asn Ala Asp Lys		35	40	45		Ser Asn Ala Val Leu Ile Cys His Ala Leu Thr Gly Asp Gln His Val		50	55	60		Ala Ser Pro His Pro Thr Thr Gly Lys Pro Gly Trp Trp Gln Arg Leu		65	70	75	80	Val Gly Pro Gly Lys Pro Leu Asp Pro Ala Arg His Phe Ile Ile Cys		85	90	95		Ser Asn Val Ile Gly Gly Cys Met Gly Ser Thr Gly Pro Ala Ser Ile									
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Gly Leu Glu Ile Ala Tyr Gln Thr Tyr Gly Gln Leu Asn Ala Asp Lys																																					
35	40	45		Ser Asn Ala Val Leu Ile Cys His Ala Leu Thr Gly Asp Gln His Val		50	55	60		Ala Ser Pro His Pro Thr Thr Gly Lys Pro Gly Trp Trp Gln Arg Leu		65	70	75	80	Val Gly Pro Gly Lys Pro Leu Asp Pro Ala Arg His Phe Ile Ile Cys		85	90	95		Ser Asn Val Ile Gly Gly Cys Met Gly Ser Thr Gly Pro Ala Ser Ile															
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Ser Asn Ala Val Leu Ile Cys His Ala Leu Thr Gly Asp Gln His Val																																					
50	55	60		Ala Ser Pro His Pro Thr Thr Gly Lys Pro Gly Trp Trp Gln Arg Leu		65	70	75	80	Val Gly Pro Gly Lys Pro Leu Asp Pro Ala Arg His Phe Ile Ile Cys		85	90	95		Ser Asn Val Ile Gly Gly Cys Met Gly Ser Thr Gly Pro Ala Ser Ile																					
60																																					
Ala Ser Pro His Pro Thr Thr Gly Lys Pro Gly Trp Trp Gln Arg Leu																																					
65	70	75	80	Val Gly Pro Gly Lys Pro Leu Asp Pro Ala Arg His Phe Ile Ile Cys		85	90	95		Ser Asn Val Ile Gly Gly Cys Met Gly Ser Thr Gly Pro Ala Ser Ile																											
75	80																																				
Val Gly Pro Gly Lys Pro Leu Asp Pro Ala Arg His Phe Ile Ile Cys																																					
85	90	95		Ser Asn Val Ile Gly Gly Cys Met Gly Ser Thr Gly Pro Ala Ser Ile																																	
95																																					
Ser Asn Val Ile Gly Gly Cys Met Gly Ser Thr Gly Pro Ala Ser Ile																																					

100	105	110
Asn Pro Ala Thr Gly Lys Thr Tyr Gly Leu Ser Phe Pro Val Ile Thr		
115	120	125
Ile Ala Asp Met Val Arg Ala Gln Ala Met Leu Val Ser Ala Leu Gly		
130	135	140
Val Glu Thr Leu Phe Ala Val Val Gly Gly Ser Met Gly Gly Met Gln		
145	150	155
160		
Val Gln Gln Trp Ala Val Asp Tyr Pro Glu Arg Met Phe Ser Ala Val		
165	170	175
Val Leu Ala Ser Ala Ser Arg His Ser Ala Gln Asn Ile Ala Phe His		
180	185	190
Glu Val Gly Arg Gln Ala Ile Met Ala Asp Pro Asp Trp Arg Gly Gly		
195	200	205
Ala Tyr Ala Glu His Gly Val Arg Pro Glu Lys Gly Leu Ala Val Ala		
210	215	220
Arg Met Ala Ala His Ile Thr Tyr Leu Ser Glu Pro Ala Leu Gln Arg		
225	230	235
240		
Lys Phe Gly Arg Glu Leu Gln Arg Asp Gly Leu Ser Trp Gly Phe Asp		
245	250	255
Ala Asp Phe Gln Val Glu Ser Tyr Leu Arg His Gln Gly Ser Ser Phe		
260	265	270
Val Asp Arg Phe Asp Ala Asn Ser Tyr Leu Tyr Ile Thr Arg Ala Met		
275	280	285
Asp Tyr Phe Asp Ile Ala Ala Ser His Gly Gly Val Leu Ala Lys Ala		
290	295	300
Phe Thr Arg Ala Arg Asn Val Arg Phe Cys Val Leu Ser Phe Ser Ser		
305	310	315
320		
Asp Trp Leu Tyr Pro Thr Ala Glu Asn Arg His Leu Val Arg Ala Leu		
325	330	335
Thr Ala Ala Gly Ala Arg Ala Ala Phe Ala Glu Ile Glu Ser Asp Lys		
340	345	350
Gly His Asp Ala Phe Leu Leu Asp Glu Pro Val Met Asp Ala Ala Leu		
355	360	365
Glu Gly Phe Leu Ala Ser Ala Glu Arg Asp Arg Gly Leu Val		
370	375	380

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 <212> DNA
 <213> Neisseria gonorrhoeae
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<221> CDS
<222> (1)..(1137)
<223> RNG00132

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 ttt gaa atg ccg ctg gtt ttg gaa aac ggt aaa act ttg ccg cgt ttc 96
 Phe Glu Met Pro Leu Val Leu Glu Asn Gly Lys Thr Leu Pro Arg Phe
 20 25 30

 gat ctg atg att gaa acc tac ggc gag ctg aat gct gaa aaa aac aat 144
 Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn
 35 40 45

 gcg gtt tta atc tgc cac gcg ctg tcg ggc aac cat cac gtt gcg ggc 192
 Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly
 50 55 60

 agg cat tcg gcg gag gat aaa tat acg ggc tgg tgg gac aat atg gtc 240
 Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val
 65 70 75 80

 ggt ccc gga aaa ccg att gat acg gaa cgt ttt ttc gtg gtc ggg ttg 288
 Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu
 85 90 95

 aac aat ctg ggc ggc tgc gac ggc agc agc ggg cct ttg tcg atc aat 336
 Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn
 100 105 110

 cct gaa acg ggc agg gaa tac ggc gcg gat ttt ccg atg gtt acg gtg 384
 Pro Glu-Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Met Val Thr Val
 115 120 125

 aag gac tgg gta aaa tca caa gcc gcg ctt gcc gat tat ctc ggc atc 432
 Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Ala Asp Tyr Leu Gly Ile
 130 135 140

 gaa caa tgg gcg gcg gtt gtc ggc ggc agc ttg ggc ggc atg cag gct 480
 Glu Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly Met Gln Ala
 145 150 155 160

 ttg cag tgg gcg att tcc tat ccc gaa cgt gtg cgc cac gcc ttg gtg 528
 Leu Gln Trp Ala Ile Ser Tyr Pro Glu Arg Val Arg His Ala Leu Val
 165 170 175

 att gcg tct gcg ccg aaa ctg tcc gcg caa aat atc gcg ttt aat gat 576
 Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Asp
 180 185 190

 gta gca cgt cag gcg att ttg acc gac ccc gat ttc aat gaa gga cat 624
 Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His.
 195 200 205

 tac cgc agc cac aac acc gtt ccc gcg cgc ggt ttg cgg att gcc cgt 672
 Tyr Arg Ser His Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg
 210 215 220

atg atg gga cac att acg tat ctt gcc gaa gac ggt ttg ggc aaa aaa Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys 225 230 235 240	720
ttc gga cgc gat ttg cgt tcc aac ggc tat caa tac ggc tat agc gtt Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Ser Val 245 250 255	768
gaa ttt gaa gta gaa tcc tat ctc cgc tat caa ggc gac aaa ttc gtc Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val 260 265 270	816
ggg cg ^g ttt gat gct aat aca tat ttg ctg atg acc aaa gct ttg gac Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp 275 280 285	864
tat ttc gat ccg gc ^g g ^c gat ttc ggc aac agc ctg acc cgc gcc gtg Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val 290 295 300	912
cag gat gtg cag gca aaa ttc ttt gtc gcc agc ttc agc acc gac tgg Gln Asp Val Gln Ala Lys Phe Phe Val Ala Ser Phe Ser Thr Asp Trp 305 310 315 320	960
cgt ttc gc ^g ccc gaa cgt tcg cac gaa ctg gtc aag gca ctg att gcc Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala 325 330 335	1008
gcc caa aaa tcc gtg cag tat atc gaa gtc aag tcc gca cac ggg cac Ala Gln Lys Ser Val Gln Tyr Ile Glu Val Lys Ser Ala His Gly His 340 345 350	1056
gat gcc ttt tta atg gaa gac gaa gcc tat atg cgc gcc gta acg gct Asp Ala Phe Leu Met Glu Asp Glu Ala Tyr Met Arg Ala Val Thr Ala 355 360 365	1104
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Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn 35 40 45
Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly 50 55 60

Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val
 65 70 75 80

Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu
 85 90 95

Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn
 100 105 110

Pro Glu Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Met Val Thr Val
 115 120 125

Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Ala Asp Tyr Leu Gly Ile
 130 135 140

Glu Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly Met Gln Ala
 145 150 155 160

Leu Gln Trp Ala Ile Ser Tyr Pro Glu Arg Val Arg His Ala Leu Val
 165 170 175

Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Asp
 180 185 190

Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His
 195 200 205

Tyr Arg Ser His Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg
 210 215 220

Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys
 225 230 235 240

Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Ser Val
 245 250 255

Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val
 260 265 270

Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp
 275 280 285

Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val
 290 295 300

Gln Asp Val Gln Ala Lys Phe Phe Val Ala Ser Phe Ser Thr Asp Trp
 305 310 315 320

Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala
 325 330 335

Ala Gln Lys Ser Val Gln Tyr Ile Glu Val Lys Ser Ala His Gly His
 340 345 350

Asp Ala Phe Leu Met Glu Asp Glu Ala Tyr Met Arg Ala Val Thr Ala
 355 360 365

Tyr Met Asn Asn Val Asp Lys Asp Cys Arg Leu
 370 375

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 <212> DNA
 <213> Neisseria meningitidis ser. A

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 <222> (1)..(1137)
 <223> RNM00815

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 10
 15

 ttt gaa atg ccg ctg gtt ttg gaa aac ggt aaa act ttg ccg cgt ttc 96
 Phe Glu Met Pro Leu Val Leu Glu Asn Gly Lys Thr Leu Pro Arg Phe
 20
 25
 30

 gat ctg atg att gaa acc tac ggc gag ctg aat gcc gaa aaa aat aat 144
 Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn
 35
 40
 45

 gcg gtt tta atc tgt cat gcg ctg tca ggc aac cat cat gtt gcg ggc 192
 Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly
 50
 55
 60

 agg cat tcg gcg gag gat aaa tat acg ggc tgg tgg gac aat atg gta 240
 Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val
 65
 70
 75
 80

 gga ccc ggc aaa ccg att gat aca gaa cgt ttt ttc gtc gtc ggt ttg 288
 Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu
 85
 90
 95

 aac aat ctg ggc ggc tgc gac ggc agc agc gga cct ttg tcg atc aat 336
 Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn
 100
 105
 110

 cct gaa acg ggc agg gaa tac ggc gcg gat ttt ccg gtc gtt acg gtc 384
 Pro Glu Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Val Val Thr Val
 115
 120
 125

 aag gac tgg gta aaa tcc caa gcc gcg ctt acc gat tat ctc ggc atc 432
 Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Thr Asp Tyr Leu Gly Ile
 130
 135
 140

 ggg caa tgg gcg gcg gtt gtc ggc ggc agc ttg ggc ggt atg cag gct 480
 Gly Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly Met Gln Ala
 145
 150
 155
 160

 ttg cag tgg acg att tcc tat ccc gag cgc gtc cgc cat gcc tta gtc 528
 Leu Gln Trp Thr Ile Ser Tyr Pro Glu Arg Val Arg His Ala Leu Val
 165
 170
 175

 att gcg tcc gcg ccg aaa ctg tcc acg caa aat atc gcg ttt aat gat 576
 Ile Ala Ser Ala Pro Lys Leu Ser Thr Gln Asn Ile Ala Phe Asn Asp
 180
 185
 190

gta gca cgt cag gcg att ttg acc gat ccc gat ttc aac gaa gga cat		624	
Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His			
195	200	205	
tac cgc agc cgc aac acc gtt ccc gct cgg ggc ttg cgg att gcc cgc		672	
Tyr Arg Ser Arg Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg			
210	215	220	
atg atg ggg cac atc acc tat ctt gcc gaa gac ggt ttg ggc aaa aaa		720	
Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys			
225	230	235	240
ttc gga cgc gat ttg cgt tcc aac ggc tat caa tac ggc tat ggc gtt		768	
Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Gly Val			
245	250	255	
gaa ttt gaa gta gaa tcc tat ctg cgc tat caa ggc gat aaa ttc gtc		816	
Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val			
260	265	270	
ggg cgg ttt gat gcc aac acc tat ttg ctg atg acc aag gct ttg gac		864	
Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp			
275	280	285	
tat ttc gat ccg gcg gcg gat ttc ggc aac agc ctg acc cgc gcc gtg		912	
Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val			
290	295	300	
cag gat gtt cag gca aaa ttc ttt gtc gcc agc ttc agc acc gat tgg		960	
Gln Asp Val Gln Ala Lys Phe Val Ala Ser Phe Ser Thr Asp Trp			
305	310	315	320
cgt ttc gcg ccc gaa cgt tcg cac gaa ctg gtc aag gcc ctg att gcc		1008	
Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala			
325	330	335	
gcc caa aaa tcc gtg cag tat atc gaa gtc aaa tcc gca cac ggg cac		1056	
Ala Gln Lys Ser Val Gln Tyr Ile Glu Val Lys Ser Ala His Gly His			
340	345	350	
gat gcc ttt tta atg gaa gac gaa gcc tat atg cgt gcg gtc gcc gcc		1104	
Asp Ala Phe Leu Met Glu Asp Glu Ala Tyr Met Arg Ala Val Ala Ala			
355	360	365	
tat atg aac aac gtt tat aag gaa tgt cag caa tga		1140	
Tyr Met Asn Asn Val Tyr Lys Glu Cys Gln Gln			
370	375		

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<211> 379
<212> PRT
<213> Neisseria meningitidis ser. A

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Phe Glu Met Pro Leu Val Leu Glu Asn Gly Lys Thr Leu Pro Arg Phe

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Asp Leu Met Ile Glu Thr Tyr Gly Glu Leu Asn Ala Glu Lys Asn Asn		
35	40	45
Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val Ala Gly		
50	55	60
Arg His Ser Ala Glu Asp Lys Tyr Thr Gly Trp Trp Asp Asn Met Val		
65	70	75
80		
Gly Pro Gly Lys Pro Ile Asp Thr Glu Arg Phe Phe Val Val Gly Leu		
85	90	95
Asn Asn Leu Gly Gly Cys Asp Gly Ser Ser Gly Pro Leu Ser Ile Asn		
100	105	110
Pro Glu Thr Gly Arg Glu Tyr Gly Ala Asp Phe Pro Val Val Thr Val		
115	120	125
Lys Asp Trp Val Lys Ser Gln Ala Ala Leu Thr Asp Tyr Leu Gly Ile		
130	135	140
Gly Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly Met Gln Ala		
145	150	155
160		
Leu Gln Trp Thr Ile Ser Tyr Pro Glu Arg Val Arg His Ala Leu Val		
165	170	175
Ile Ala Ser Ala Pro Lys Leu Ser Thr Gln Asn Ile Ala Phe Asn Asp		
180	185	190
Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe Asn Glu Gly His		
195	200	205
Tyr Arg Ser Arg Asn Thr Val Pro Ala Arg Gly Leu Arg Ile Ala Arg		
210	215	220
Met Met Gly His Ile Thr Tyr Leu Ala Glu Asp Gly Leu Gly Lys Lys		
225	230	235
240		
Phe Gly Arg Asp Leu Arg Ser Asn Gly Tyr Gln Tyr Gly Tyr Gly Val		
245	250	255
Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys Phe Val		
260	265	270
Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala Leu Asp		
275	280	285
Tyr Phe Asp Pro Ala Ala Asp Phe Gly Asn Ser Leu Thr Arg Ala Val		
290	295	300
Gln Asp Val Gln Ala Lys Phe Phe Val Ala Ser Phe Ser Thr Asp Trp		
305	310	315
320		
Arg Phe Ala Pro Glu Arg Ser His Glu Leu Val Lys Ala Leu Ile Ala		
325	330	335
Ala Gln Lys Ser Val Gln Tyr Ile Glu Val Lys Ser Ala His Gly His		

340

345

350

Asp Ala Phe Leu Met Glu Asp Glu Ala Tyr Met Arg Ala Val Ala Ala
 355 360 365

Tyr Met Asn Asn Val Tyr Lys Glu Cys Gln Gln
 370 375

<210> 15
 <211> 1140
 <212> DNA
 <213> Pseudomonas fluorescens

<220>
 <221> CDS
 <222> (1)...(1137)
 <223> RPU01633

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 Met Pro Ala Ala Phe Pro Pro Asp Ser Val Gly Leu Val Thr Pro Gln
 1 5 10 15

acg gcg cac ttc agc gaa ccg ctg gcc ctg gcc tgc ggc cgt tcg ctg 96
 Thr Ala His Phe Ser Glu Pro Leu Ala Leu Ala Cys Gly Arg Ser Leu
 20 25 30

gcc gat tat gac ctg atc tac gaa acc tac ggc acg ctg aac gcg caa 144
 Ala Asp Tyr Asp Leu Ile Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Gln
 35 40 45

gcg agc aac gcc gtg ctg atc tgc cac gcc ttg tcc ggc cac cac cat 192
 Ala Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His
 50 55 60

gct gcg ggt tat cac agc gtc gac gac cgc aag ccc ggt tgg tgg gac 240
 Ala Ala Gly Tyr His Ser Val Asp Asp Arg Lys Pro Gly Trp Trp Asp
 65 70 75 80

agc tgc atc ggc ccc ggc aaa ccg atc gac acc aac aag ttc ttc gtg 288
 Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Asn Lys Phe Phe Val
 85 90 95

gtc agc ctg aac aac ctc ggc ggt tgc aat ggt tct acc ggc ccg agc 336
 Val Ser Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Thr Gly Pro Ser
 100 105 110

agc ctc aat ccg gaa acc ggc aag ccg ttc ggc gcc gac ttc ccg gtg 384
 Ser Leu Asn Pro Glu Thr Gly Lys Pro Phe Gly Ala Asp Phe Pro Val
 115 120 125

ctg acc gtg gaa gac tgg gtg cac agc cag gca cgc ctg gcc gac ctg 432
 Leu Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Leu
 130 135 140

ctc ggc atc ggc cag tgg gcg gcg gtg atc ggc ggc agc ctg ggc ggc 480
 Leu Gly Ile Gly Gln Trp Ala Ala Val Ile Gly Gly Ser Leu Gly Gly
 145 150 155 160

atg cag gcg ctg caa tgg acc atc acc tat ccg gat cgc gtt cgc cac Met Gln Ala Leu Gln Trp Thr Ile Thr Tyr Pro Asp Arg Val Arg His 165	170	175	528	
tgc ctg gcc atc gcc tcg gcc ccc aag ctg tcg gcg cag aac atc gcc Cys Leu Ala Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala 180	185	190	576	
ttc aac gaa gtg gcg cgc cag gcg atc ctc act gac ccg gaa ttc cac Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Glu Phe His 195	200	205	624	
ggc ggc tcg ttc cag gaa cac ggc gtg atc ccc aag cgc ggc ctg atg Gly Gly Ser Phe Gln Glu His Gly Val Ile Pro Lys Arg Gly Leu Met 210	215	220	672	
ctg gcg cgg atg gtg ggg cac atc acc tac ctg tcc gac gac tcc atg Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met 225	230	235	240	720
ggt gag aaa ttc ggc cgt ggc ctg aag agc gaa aag ctc aac tac gac Gly Glu Lys Phe Gly Arg Gly Leu Lys Ser Glu Lys Leu Asn Tyr Asp 245	250	255	768	
ttc cac agc gtc gag ttc cag gtc gaa agc tac ctg cgc tat cag ggc Phe His Ser Val Glu Phe Gln Val Glu Ser Tyr Leu Arg Tyr Gln Gly 260	265	270	816	
gaa gag ttc tcc ggg cgc ttc gat gcc aac acc tat ctg ttg atg acc Glu Glu Phe Ser Gly Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr 275	280	285	864	
aag gcg ctg gac tac ttc gat ccg gcg gcg aac ttc aac gat aac ctg Lys Ala Leu Asp Tyr Phe Asp Pro Ala Ala Asn Phe Asn Asp Asn Leu 290	295	300	912	
gcg aaa acc ttc gaa ggt gca aaa gcc aag ttc tgc gtg atg tcg ttc Ala Lys Thr Phe Glu Gly Ala Lys Ala Phe Cys Val Met Ser Phe 305	310	315	320	960
acc acc gac tgg cgc ttc tcc ccg gcc cgc tcg cga gaa ctg gtg gat Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Leu Val Asp 325	330	335	1008	
gcg ctg atg gcg gcg cgc aaa gac gtc agc tac ctg gaa atc gac gcg Ala Leu Met Ala Ala Arg Lys Asp Val Ser Tyr Leu Glu Ile Asp Ala 340	345	350	1056	
ccc cag ggc cac gac gcc ttc ctg att ccg atc ccg cgc tac ttg cag Pro Gln Gly His Asp Ala Phe Leu Ile Pro Ile Pro Arg Tyr Leu Gln 355	360	365	1104	
gcg ttc ggc aat tac atg aac cgc att acg ttg tga Ala Phe Gly Asn Tyr Met Asn Arg Ile Thr Leu 370	375		1140	

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<211> 379
<212> PRT

<213> Pseudomonas fluorescens

<400> 16

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Thr	Ala	His	Phe	Ser	Glu	Pro	Leu	Ala	Leu	Ala	Cys	Gly	Arg	Ser	Leu
				20				25				30			

Ala	Asp	Tyr	Asp	Leu	Ile	Tyr	Glu	Thr	Tyr	Gly	Thr	Leu	Asn	Ala	Gln
				35			40				45				

Ala	Ser	Asn	Ala	Val	Leu	Ile	Cys	His	Ala	Leu	Ser	Gly	His	His	His
				50			55			60					

Ala	Ala	Gly	Tyr	His	Ser	Val	Asp	Asp	Arg	Lys	Pro	Gly	Trp	Trp	Asp
				65			70			75			80		

Ser	Cys	Ile	Gly	Pro	Gly	Lys	Pro	Ile	Asp	Thr	Asn	Lys	Phe	Phe	Val
				85				90				95			

Val	Ser	Leu	Asn	Asn	Leu	Gly	Gly	Cys	Asn	Gly	Ser	Thr	Gly	Pro	Ser
					100			105			110				

Ser	Leu	Asn	Pro	Glu	Thr	Gly	Lys	Pro	Phe	Gly	Ala	Asp	Phe	Pro	Val
				115			120			125					

Leu	Thr	Val	Glu	Asp	Trp	Val	His	Ser	Gln	Ala	Arg	Leu	Ala	Asp	Leu
					130			135			140				

Leu	Gly	Ile	Gly	Gln	Trp	Ala	Ala	Val	Ile	Gly	Gly	Ser	Leu	Gly	Gly
					145			150			155			160	

Met	Gln	Ala	Leu	Gln	Trp	Thr	Ile	Thr	Tyr	Pro	Asp	Arg	Val	Arg	His
					165			170			175				

Cys	Leu	Ala	Ile	Ala	Ser	Ala	Pro	Lys	Leu	Ser	Ala	Gln	Asn	Ile	Ala
					180			185			190				

Phe	Asn	Glu	Val	Ala	Arg	Gln	Ala	Ile	Leu	Thr	Asp	Pro	Glu	Phe	His
					195			200			205				

Gly	Gly	Ser	Phe	Gln	Glu	His	Gly	Val	Ile	Pro	Lys	Arg	Gly	Leu	Met
					210			215			220				

Leu	Ala	Arg	Met	Val	Gly	His	Ile	Thr	Tyr	Leu	Ser	Asp	Asp	Ser	Met
					225			230			235			240	

Gly	Glu	Lys	Phe	Gly	Arg	Gly	Leu	Lys	Ser	Glu	Lys	Leu	Asn	Tyr	Asp
					245			250			255				

Phe	His	Ser	Val	Glu	Phe	Gln	Val	Glu	Ser	Tyr	Leu	Arg	Tyr	Gln	Gly
					260			265			270				

Glu	Glu	Phe	Ser	Gly	Arg	Phe	Asp	Ala	Asn	Thr	Tyr	Leu	Leu	Met	Thr
					275			280			285				

Lys	Ala	Leu	Asp	Tyr	Phe	Asp	Pro	Ala	Ala	Asn	Phe	Asn	Asp	Asn	Leu
					290			295			300				

Ala Lys Thr Phe Glu Gly Ala Lys Ala Lys Phe Cys Val Met Ser Phe
 305 310 315 320

Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Leu Val Asp
 325 330 335

Ala Leu Met Ala Ala Arg Lys Asp Val Ser Tyr Leu Glu Ile Asp Ala
 340 345 350

Pro Gln Gly His Asp Ala Phe Leu Ile Pro Ile Pro Arg Tyr Leu Gln
 355 360 365

Ala Phe Gly Asn Tyr Met Asn Arg Ile Thr Leu
 370 375

<210> 17

<211> 1140

<212> DNA

<213> Pseudomonas aeruginosa

<220>

<221> CDS

<222> (1)..(1137)

<223> RPA04460

<400> 17

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Met	Pro	Thr	Val	Phe	Pro	Asp	Asp	Ser	Val	Gly	Leu	Val	Ser	Pro	Gln		
1	5							10					15				

acg	ctg	cac	tcc	aac	gaa	ccg	ctc	gag	ctg	acc	agc	ggc	aag	tcc	ctg		96
Thr	Leu	His	Phe	Asn	Glu	Pro	Leu	Glu	Leu	Thr	Ser	Gly	Lys	Ser	Leu		
20	25								30								

gcc	gag	tac	gac	ctg	gtg	atc	gaa	acc	tac	ggc	gag	ctg	aat	gcc	acg		144
Ala	Glu	Tyr	Asp	Leu	Val	Ile	Glu	Thr	Tyr	Gly	Glu	Leu	Asn	Ala	Thr		
35	40								45								

cag	agc	aac	gcg	gtg	ctg	atc	tgc	cac	gcc	ctc	tcc	ggc	cac	cac	cac		192
Gln	Ser	Asn	Ala	Val	Ile	Cys	His	Ala	Leu	Ser	Gly	His	Leu	Asn	Ala	Thr	
50	55							60									

gcc	gcc	ggc	tac	cac	agc	gtc	gac	gag	cgc	aag	ccg	ggc	tgg	tgg	gac		240
Ala	Ala	Gly	Tyr	His	Ser	Val	Asp	Glu	Arg	Lys	Pro	Gly	Trp	Trp	Asp		
65	70							75		80							

agc	tgc	atc	ggc	ggc	aag	ccg	atc	gac	acc	cgc	aag	tcc	tcc	gtc		288
Ser	Cys	Ile	Gly	Pro	Lys	Pro	Ile	Asp	Thr	Arg	Lys	Phe	Phe	Val		
85	90								95							

gtc	gcc	ctc	aac	aac	ctc	ggc	ggt	tgc	aac	gga	tcc	agc	ggc	ccc	gcc		336
Val	Ala	Leu	Asn	Asn	Leu	Gly	Gly	Cys	Asn	Gly	Ser	Ser	Gly	Pro	Ala		
100	105								110								

agc	atc	aat	ccg	gcg	acc	ggc	aag	gtc	tac	ggc	gac	ttc	ccg	atg		384
Ser	Ile	Asn	Pro	Ala	Thr	Gly	Lys	Val	Tyr	Gly	Ala	Asp	Phe	Pro	Met	
115	120								125							

gtt	acg	gtg	gaa	gac	tgg	gtg	cat	agc	cag	gcg	cgc	ctg	gca	gac	cgc		432
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Val Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg			
130	135	140	
ctc ggc atc cgc cag tgg gcc gcg gtg gtc ggc ggc agc ctc ggc ggc	480		
Leu Gly Ile Arg Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly			
145	150	155	160
atg cag gcg ctg caa tgg acc atc agc tat ccc gag cgc gtc cgt cac	528		
Met Gln Ala Leu Gln Trp Thr Ile Ser Tyr Pro Glu Arg Val Arg His			
165	170	175	
tgc ctg tgc atc gcc agc gcg ccg aag ctg tcg gcg cag aac atc gcc	576		
Cys Leu Cys Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala			
180	185	190	
ttc aac gaa gtc gcc cg ^g cag g ^g att ctt tcc gac cct gag ttc ctc	624		
Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Ser Asp Pro Glu Phe Leu			
195	200	205	
ggc ggc tac ttc cag gag cag ggc gtg att ccc aag cgc ggc ctc aag	672		
Gly Gly Tyr Phe Gln Glu Gln Gly Val Ile Pro Lys Arg Gly Leu Lys			
210	215	220	
ctg gcg cgg atg gtc ggc cat atc acc tac ctg tcc gac gac gcc atg	720		
Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ala Met			
225	230	235	240
ggc gcc aag ttc ggc cgt gta ctg aag acc gag aag ctc aac tac gac	768		
Gly Ala Lys Phe Gly Arg Val Leu Lys Thr Glu Lys Leu Asn Tyr Asp			
245	250	255	
ctg cac agc gtc gag ttc cag gtc gag agt tac ctg cgc tac cag ggc	816		
Leu His Ser Val Glu Phe Gln Val Glu Ser Tyr Leu Arg Tyr Gln Gly			
260	265	270	
gag gag ttc tcc acc cgc ttc gac gcc aat acc tac ctg ctg atg acc	864		
Glu Glu Phe Ser Thr Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr			
275	280	285	
aag gcg ctg gac tac ttc gac ccc gcc gcc cac ggc gac gac ctg	912		
Lys Ala Leu Asp Tyr Phe Asp Pro Ala Ala Ala His Gly Asp Asp Leu			
290	295	300	
gtg cgc acc ctg gag ggc gtc gag g ^g c ^g gac ttc tgc ctg atg tcc ttc	960		
Val Arg Thr Leu Glu Gly Val Glu Ala Asp Phe Cys Leu Met Ser Phe			
305	310	315	320
acc acc gac tgg cgt ttc tcg ccg gcc cgc tcg cgg gaa atc gtc gac	1008		
Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Ile Val Asp			
325	330	335	
gcc ctg atc gcg gcg aaa aag aac gtc agc tac ctg gag atc gac gcc	1056		
Ala Leu Ile Ala Ala Lys Lys Asn Val Ser Tyr Leu Glu Ile Asp Ala			
340	345	350	
ccg caa ggc cac gac gcc ttc ctc atg ccg atc ccc cgg tac ctg caa	1104		
Pro Gln Gly His Asp Ala Phe Leu Met Pro Ile Pro Arg Tyr Leu Gln			
355	360	365	
gcc ttc agc ggt tac atg aac cgc atc agc gtg tga	1140		

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370 375

<210> 18
<211> 379
<212> PRT
<213> Pseudomonas aeruginosa

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35 40 45

Gln Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His
50 55 60

Ala Ala Gly Tyr His Ser Val Asp Glu Arg Lys Pro Gly Trp Trp Asp
65 70 75 80

Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Arg Lys Phe Phe Val
85 90 95

Val Ala Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Ser Gly Pro Ala
100 105 110

Ser Ile Asn Pro Ala Thr Gly Lys Val Tyr Gly Ala Asp Phe Pro Met
115 120 125

Val Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg
130 135 140

Leu Gly Ile Arg Gln Trp Ala Ala Val Val Gly Gly Ser Leu Gly Gly
145 150 155 160

Met Gln Ala Leu Gln Trp Thr Ile Ser Tyr Pro Glu Arg Val Arg His
165 170 175

Cys Leu Cys Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala
180 185 190

Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Ser Asp Pro Glu Phe Leu
195 200 205

Gly Gly Tyr Phe Gln Glu Gln Gly Val Ile Pro Lys Arg Gly Leu Lys
210 215 220

Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ala Met
225 230 235 240

Gly Ala Lys Phe Gly Arg Val Leu Lys Thr Glu Lys Leu Asn Tyr Asp
245 250 255

Leu His Ser Val Glu Phe Gln Val Glu Ser Tyr Leu Arg Tyr Gln Gly
260 265 270

Glu Glu Phe Ser Thr Arg Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr
 275 280 285

Lys Ala Leu Asp Tyr Phe Asp Pro Ala Ala Ala His Gly Asp Asp Leu
 290 295 300

Val Arg Thr Leu Glu Gly Val Glu Ala Asp Phe Cys Leu Met Ser Phe
 305 310 315 320

Thr Thr Asp Trp Arg Phe Ser Pro Ala Arg Ser Arg Glu Ile Val Asp
 325 330 335

Ala Leu Ile Ala Ala Lys Lys Asn Val Ser Tyr Leu Glu Ile Asp Ala
 340 345 350

Pro Gln Gly His Asp Ala Phe Leu Met Pro Ile Pro Arg Tyr Leu Gln
 355 360 365

Ala Phe Ser Gly Tyr Met Asn Arg Ile Ser Val
 370 375

<210> 19

<211> 1146

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (1)..(1143)

<223> RBU12675

<400> 19

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ccg ctg ccg ttg cag aac ggc agt tcg ctc gcc ggt tac gac ctg atg	96
Pro Leu Pro Leu Gln Asn Gly Ser Ser Leu Ala Gly Tyr Asp Leu Met	
20 25 30	

gtc gag acc tac ggc acg ctc aac gcc gcg cgt agc aac gcg gtg ctg	144
Val Glu Thr Tyr Gly Thr Leu Asn Ala Ala Arg Ser Asn Ala Val Leu	
35 40 45	

gtg tgc cac gcg ctc aac gcg tcg cac cac gtg gcg ggc gtg tat gcc	192
Val Cys His Ala Leu Asn Ala Ser His His Val Ala Gly Val Tyr Ala	
50 55 60	

gac aac ccc agg gac atc ggc tgg tgg gac aac atg gtc ggc ccg ggc	240
Asp Asn Pro Arg Asp Ile Gly Trp Trp Asp Asn Met Val Gly Pro Gly	
65 70 75 80	

aag ccg ctc gac act gac aag ttc ttc gtg atc ggc gtg aac aac ctc	288
Lys Pro Leu Asp Thr Asp Lys Phe Phe Val Ile Gly Val Asn Asn Leu	
85 90 95	

gga tcg tgc ttc ggc tcg act ggg ccg atg agc atc gat ccg tct acc	336
Gly Ser Cys Phe Gly Ser Thr Gly Pro Met Ser Ile Asp Pro Ser Thr	

100

105

110

ggc aat ccg tac ggc gcg acg ttt ccc gtc gtg acg gtg gaa gac gac tgg Gly Asn Pro Tyr Gly Ala Thr Phe Pro Val Val Thr Val Glu Asp Trp	384		
115	120	125	
gtc aac gcc cag gcg cgc gtc gcg gat caa ttc ggc atc acg cgc ttt Val Asn Ala Gln Ala Arg Val Ala Asp Gln Phe Gly Ile Thr Arg Phe	432		
130	135	140	
gcg gcg gtg atg ggc ggc agc ctc ggc ggc atg cag gcg ctc gcg tgg Ala Ala Val Met Gly Gly Ser Leu Gly Gly Met Gln Ala Leu Ala Trp	480		
145	150	155	160
agc atg atg tat ccg gag cgc gtc gct cac tgc atc gtg gtc gcg tcc Ser Met Met Tyr Pro Glu Arg Val Ala His Cys Ile Val Val Ala Ser	528		
165	170	175	
aca ccc aag ctg tcg gcg cag aac atc gcg ttc aac gag gtt gcg cgc Thr Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Glu Val Ala Arg	576		
180	185	190	
tcg gcg atc ctg tcg gac ccg gac ttc cac ggc ggc aac tac tac gcg Ser Ala Ile Leu Ser Asp Pro Asp Phe His Gly Gly Asn Tyr Tyr Ala	624		
195	200	205	
cac aac gtt aag ccg aag cgc ggc ctg cgc gtc gcg cgc atg atc ggc His Asn Val Lys Pro Lys Arg Gly Leu Arg Val Ala Arg Met Ile Gly	672		
210	215	220	
cac atc acg tat ctg tcg gac gac atg gcc gag aaa ttc ggc cgc His Ile Thr Tyr Leu Ser Asp Asp Met Ala Glu Lys Phe Gly Arg	720		
225	230	235	240
tcg ctg cgg cgc gcg gaa ggc gcg ctg gac gcg tac aac ttc aac ttc Ser Leu Arg Arg Ala Glu Gly Ala Leu Asp Ala Tyr Asn Phe Asn Phe	768		
245	250	255	
gac gtg gag ttc gag gtg gag tcg tac ctg cgc tac cag ggc gac aag Asp Val Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys	816		
260	265	270	
tcc gcc gac tac ttc gac gcg aat acg tat ctg ctg atc acc cgc gcg Phe Ala Asp Tyr Phe Asp Ala Asn Thr Tyr Leu Leu Ile Thr Arg Ala	864		
275	280	285	
ctc gac tac ttc gat ccg gcc aag gcc ttc gcc ggc gac ctg acg gcc Leu Asp Tyr Phe Asp Pro Ala Lys Ala Phe Ala Gly Asp Leu Thr Ala	912		
290	295	300	
gcg gtc gcg cac acc acg gcg aaa tat ctg atc gcc agc ttc acg acc Ala Val Ala His Thr Thr Ala Lys Tyr Leu Ile Ala Ser Phe Thr Thr	960		
305	310	315	320
gac tgg cgc ttc gcg ccg gcc cgc tcg cgt gaa ctg gtg aag gcg ctg Asp Trp Arg Phe Ala Pro Ala Arg Ser Arg Glu Leu Val Lys Ala Leu	1008		
325	330	335	
ctc gat cac aag cgc acg gtc acc tac gcg gaa atc gac gcg ccg cac Leu Asp His Lys Arg Thr Val Thr Tyr Ala Glu Ile Asp Ala Pro His	1056		

340

345

350

ggc cac gac gcc ttc ctg ctc gac gac gcg cg_c tat cac aac ctg atg 1104
 Gly His Asp Ala Phe Leu Leu Asp Asp Ala Arg Tyr His Asn Leu Met
 355 360 365

cg_c gct tac tac gaa cgt att gcg aac gag gtg aac gca tga 1146
 Arg Ala Tyr Tyr Glu Arg Ile Ala Asn Glu Val Asn Ala
 370 375 380

<210> 20
 <211> 381
 <212> PRT
 <213> Burkholderia cepacia

<400> 20
 Met Glu Ser Ile Gly Ile Val Ala Pro Gln Lys Met His Phe Thr Glu
 1 5 10 15

Pro Leu Pro Leu Gln Asn Gly Ser Ser Leu Ala Gly Tyr Asp Leu Met
 20 25 30

Val Glu Thr Tyr Gly Thr Leu Asn Ala Ala Arg Ser Asn Ala Val Leu
 35 40 45

Val Cys His Ala Leu Asn Ala Ser His His Val Ala Gly Val Tyr Ala
 50 55 60

Asp Asn Pro Arg Asp Ile Gly Trp Trp Asp Asn Met Val Gly Pro Gly
 65 70 75 80

Lys Pro Leu Asp Thr Asp Lys Phe Phe Val Ile Gly Val Asn Asn Leu
 85 90 95

Gly Ser Cys Phe Gly Ser Thr Gly Pro Met Ser Ile Asp Pro Ser Thr
 100 105 110

Gly Asn Pro Tyr Gly Ala Thr Phe Pro Val Val Thr Val Glu Asp Trp
 115 120 125

Val Asn Ala Gln Ala Arg Val Ala Asp Gln Phe Gly Ile Thr Arg Phe
 130 135 140

Ala Ala Val Met Gly Gly Ser Leu Gly Gly Met Gln Ala Leu Ala Trp
 145 150 155 160

Ser Met Met Tyr Pro Glu Arg Val Ala His Cys Ile Val Val Ala Ser
 165 170 175

Thr Pro Lys Leu Ser Ala Gln Asn Ile Ala Phe Asn Glu Val Ala Arg
 180 185 190

Ser Ala Ile Leu Ser Asp Pro Asp Phe His Gly Gly Asn Tyr Tyr Ala
 195 200 205

His Asn Val Lys Pro Lys Arg Gly Leu Arg Val Ala Arg Met Ile Gly
 210 215 220

His Ile Thr Tyr Leu Ser Asp Asp Met Ala Glu Lys Phe Gly Arg

225

230

235

240

Ser Leu Arg Arg Ala Glu Gly Ala Leu Asp Ala Tyr Asn Phe Asn Phe
 245 250 255

Asp Val Glu Phe Glu Val Glu Ser Tyr Leu Arg Tyr Gln Gly Asp Lys
 260 265 270

Phe Ala Asp Tyr Phe Asp Ala Asn Thr Tyr Leu Leu Ile Thr Arg Ala
 275 280 285

Leu Asp Tyr Phe Asp Pro Ala Lys Ala Phe Ala Gly Asp Leu Thr Ala
 290 295 300

Ala Val Ala His Thr Thr Ala Lys Tyr Leu Ile Ala Ser Phe Thr Thr
 305 310 315 320

Asp Trp Arg Phe Ala Pro Ala Arg Ser Arg Glu Leu Val Lys Ala Leu
 325 330 335

Leu Asp His Lys Arg Thr Val Thr Tyr Ala Glu Ile Asp Ala Pro His
 340 345 350

Gly His Asp Ala Phe Leu Leu Asp Asp Ala Arg Tyr His Asn Leu Met
 355 360 365

Arg Ala Tyr Tyr Glu Arg Ile Ala Asn Glu Val Asn Ala
 370 375 380

<210> 21
 <211> 1134
 <212> DNA
 <213> Nitrosomonas europaea

<220>
 <221> CDS
 <222> (1)..(1131)
 <223> RNE02005

<400> 21
 atg tcc aca caa gat tct gat tcg atc ggc atc gta tcg gca cga cgc 48
 Met Ser Thr Gln Asp Ser Asp Ser Ile Gly Ile Val Ser Ala Arg Arg
 1 5 10 15

gcc cat ttc gac acc ccg ctc agc ctg aaa agc gga gct gta ctg gac 96
 Ala His Phe Asp Thr Pro Leu Ser Leu Lys Ser Gly Ala Val Leu Asp
 20 25 30

agc tac gag ctc gtc tat gaa acc tat ggg gag ctg aat gca gac cga 144
 Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Glu Leu Asn Ala Asp Arg
 35 40 45

tcc aat gca gtg ctg atc tgc cat gct tta tcc ggc aac cac cat gtt 192
 Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val
 50 55 60

gcc ggt gtt tat gca gat aac ccc aag aat acc gga tgg tgg aac aac 240
 Ala Gly Val Tyr Ala Asp Asn Pro Lys Asn Thr Gly Trp Trp Asn Asn
 65 70 75 80

atg atc ggt ccg ggc aaa ccg gtc gat acc cga aaa ttc ttt gtc atc Met Ile Gly Pro Gly Lys Pro Val Asp Thr Arg Lys Phe Phe Val Ile 85 90 95	288
ggt atc aat aat ctc ggg ggt tgc cat ggc tcc acc ggg ccc atc agc Gly Ile Asn Asn Leu Gly Cys His Gly Ser Thr Gly Pro Ile Ser 100 105 110	336
atc aac gac aag acc ggt aaa cgc ttc ggc ccg gat ttt ccg ctg gta Ile Asn Asp Lys Thr Gly Lys Arg Phe Gly Pro Asp Phe Pro Leu Val 115 120 125	384
acg aca gct gac tgg gca aaa acc tat gtc cgt ttc gcc gat cag ttc Thr Thr Ala Asp Trp Ala Lys Thr Tyr Val Arg Phe Ala Asp Gln Phe 130 135 140	432
agc atc gac tgt ttt gcc gtc atc ggt ggc agt ctg ggc ggg atg Ser Ile Asp Cys Phe Ala Ala Val Ile Gly Ser Leu Gly Gly Met 145 150 155 160	480
tcg gcc atg caa ctg gcg ctc gat gca ccg gaa aga gtt cgt cat gcc Ser Ala Met Gln Leu Ala Leu Asp Ala Pro Glu Arg Val Arg His Ala 165 170 175	528
ata gtg gtt gca gca tcg gcc agg ctg aca gca cag aac atc gct ttc Ile Val Val Ala Ala Ser Ala Arg Leu Thr Ala Gln Asn Ile Ala Phe 180 185 190	576
aat gat gtc gcg cgt cag gcg att ctg acc gac cct gat ttt cac gac Asn Asp Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe His Asp 195 200 205	624
ggc gac tat tat tcc cat ggc acc cac ccg cgc aga ggt tta cgc ctt Gly Asp Tyr Tyr Ser His Gly Thr His Pro Arg Arg Gly Leu Arg Leu 210 215 220	672
gcc cgc atg ctt ggc cac atc acc tac ctg tcg gac gac tcc atg gcc Ala Arg Met Leu Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met Ala 225 230 235 240	720
agc aaa ttc ggc cgt gag tta cgt aac ggc tcg ctt gct ttc aat tat Ser Lys Phe Gly Arg Glu Leu Arg Asn Gly Ser Leu Ala Phe Asn Tyr 245 250 255	768
gat gtg gaa ttc cag atc gaa tcc tat ctg cac cat cag ggc gac aaa Asp Val Glu Phe Gln Ile Glu Ser Tyr Leu His His Gln Gly Asp Lys 260 265 270	816
ttt gcc gac ctg ttc gac gca aac act tat ctg ctg atg acg aag gcg Phe Ala Asp Leu Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala 275 280 285	864
ctc gat tat ttc gat ccg gcc cag gat tac gat ggc aac ctg agt gca Leu Asp Tyr Phe Asp Pro Ala Gln Asp Tyr Asp Gly Asn Leu Ser Ala 290 295 300	912
gcc ttt gcc cgt gca caa gcg gat ttt ctg gta ctt tcc ttt act tcc Ala Phe Ala Arg Ala Gln Ala Asp Phe Leu Val Leu Ser Phe Thr Ser 305 310 315 320	960

gac tgg cgt ttt tcc ccg gag cgt tcg cgc gat atc gtc aag gca ctg 1008
 Asp Trp Arg Phe Ser Pro Glu Arg Ser Arg Asp Ile Val Lys Ala Leu
 325 330 335

ctc gac aac aaa ctg aat gtc agt tat gcg gaa att ccc tcc tcg tac 1056
 Leu Asp Asn Lys Leu Asn Val Ser Tyr Ala Glu Ile Pro Ser Ser Tyr
 340 345 350

gga cat gat tcc ttt ctc atg cag gac gac tac tat cac cag ttg ata 1104
 Gly His Asp Ser Phe Leu Met Gln Asp Asp Tyr Tyr His Gln Leu Ile
 355 360 365

cgt gct tac atg aac aat atc gct ctc tag 1134
 Arg Ala Tyr Met Asn Asn Ile Ala Leu
 370 375

<210> 22
<211> 377
<212> PRT
<213> Nitrosomonas europaea

<400> 22
Met Ser Thr Gln Asp Ser Asp Ser Ile Gly Ile Val Ser Ala Arg Arg
 1 5 10 15

Ala His Phe Asp Thr Pro Leu Ser Leu Lys Ser Gly Ala Val Leu Asp
 20 25 30

Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Glu Leu Asn Ala Asp Arg
 35 40 45

Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly Asn His His Val
 -50 55 60 *

Ala Gly Val Tyr Ala Asp Asn Pro Lys Asn Thr Gly Trp Trp Asn Asn
 65 70 75 80

Met Ile Gly Pro Gly Lys Pro Val Asp Thr Arg Lys Phe Phe Val Ile
 85 90 95

Gly Ile Asn Asn Leu Gly Gly Cys His Gly Ser Thr Gly Pro Ile Ser
 100 105 110

Ile Asn Asp Lys Thr Gly Lys Arg Phe Gly Pro Asp Phe Pro Leu Val
 115 120 125

Thr Thr Ala Asp Trp Ala Lys Thr Tyr Val Arg Phe Ala Asp Gln Phe
 130 135 140

Ser Ile Asp Cys Phe Ala Ala Val Ile Gly Gly Ser Leu Gly Gly Met
 145 150 155 160

Ser Ala Met Gln Leu Ala Leu Asp Ala Pro Glu Arg Val Arg His Ala
 165 170 175

Ile Val Val Ala Ala Ser Ala Arg Leu Thr Ala Gln Asn Ile Ala Phe
 180 185 190

Asn Asp Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Asp Phe His Asp
 195 200 205

Gly Asp Tyr Tyr Ser His Gly Thr His Pro Arg Arg Gly Leu Arg Leu
 210 215 220

Ala Arg Met Leu Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met Ala
 225 230 235 240

Ser Lys Phe Gly Arg Glu Leu Arg Asn Gly Ser Leu Ala Phe Asn Tyr
 245 250 255

Asp Val Glu Phe Gln Ile Glu Ser Tyr Leu His His Gln Gly Asp Lys
 260 265 270

Phe Ala Asp Leu Phe Asp Ala Asn Thr Tyr Leu Leu Met Thr Lys Ala
 275 280 285

Leu Asp Tyr Phe Asp Pro Ala Gln Asp Tyr Asp Gly Asn Leu Ser Ala
 290 295 300

Ala Phe Ala Arg Ala Gln Ala Asp Phe Leu Val Leu Ser Phe Thr Ser
 305 310 315 320

Asp Trp Arg Phe Ser Pro Glu Arg Ser Arg Asp Ile Val Lys Ala Leu
 325 330 335

Leu Asp Asn Lys Leu Asn Val Ser Tyr Ala Glu Ile Pro Ser Ser Tyr
 340 345 350

Gly His Asp Ser Phe Leu Met Gln Asp Asp Tyr Tyr His Gln Leu Ile
 355 360 365

Arg Ala Tyr Met Asn Asn Ile Ala Leu
 370 375

<210> 23
<211> 1077
<212> DNA
<213> Haemophilus influenzae

<220>
<221> CDS
<222> (1)..(1074)
<223> RHI02681

<400> 23
atg tct gtg caa aat gta gtg ctt ttt gac aca cag cct tta act ctg 48
Met Ser Val Gln Asn Val Val Leu Phe Asp Thr Gln Pro Leu Thr Leu
 1 5 10 15

atg ctt ggc ggc aaa ctt tcc cat att aat gtc gcg tat caa act tat 96
Met Leu Gly Gly Lys Leu Ser His Ile Asn Val Ala Tyr Gln Thr Tyr
 20 25 30

ggc acg ctc aat gcc gaa aaa aat aat gcg gta tta att tgc cac gct 144
Gly Thr Leu Asn Ala Glu Lys Asn Asn Ala Val Leu Ile Cys His Ala
 35 40 45

ttg act ggt gat gct gag cct tat ttc gat gat ggt cga gat ggc tgg Leu Thr Gly Asp Ala Glu Pro Tyr Phe Asp Asp Gly Arg Asp Gly Trp	50	55	60	192
tgg cag aat ttt atg gga gca ggt tta gca ttg gat acg gat cgt tat Trp Gln Asn Phe Met Gly Ala Gly Leu Ala Leu Asp Thr Asp Arg Tyr	65	70	75	80
ttt ttt att agc tcg aac gta tta ggt ggt tgc aag gga aca act ggg Phe Phe Ile Ser Ser Asn Val Leu Gly Gly Cys Lys Gly Thr Thr Gly	85	90	95	288
cct tca tca att aat ccg caa acg ggt aaa cct tat ggc agc caa ttt Pro Ser Ser Ile Asn Pro Gln Thr Gly Lys Pro Tyr Gly Ser Gln Phe	100	105	110	336
cct aat att gtt gtg caa gat att gtt aaa gta caa aaa gcc ttg ctt Pro Asn Ile Val Val Gln Asp Ile Val Lys Val Gln Lys Ala Leu Leu	115	120	125	384
gat cat ctt ggt att agc cat tta aaa gcc att att ggt gga tct ttt Asp His Leu Gly Ile Ser His Leu Lys Ala Ile Ile Gly Gly Ser Phe	130	135	140	432
ggc ggc atg caa gcg aat caa tgg gcg att gat tat cct gat ttt atg Gly Gly Met Gln Ala Asn Gln Trp Ala Ile Asp Tyr Pro Asp Phe Met	145	150	155	160
gat aat atc gtg aat ctt tgc tca tcc att tat ttt agt gct gaa gcc Asp Asn Ile Val Asn Leu Cys Ser Ser Ile Tyr Phe Ser Ala Glu Ala	165	170	175	528
ata ggt ttt aat cac gta atg cgt caa gcg gtc att aat gat ccc aat Ile Gly Phe Asn His Val Met Arg Gln Ala Val Ile Asn Asp Pro Asn	180	185	190	576
ttt aac ggc ggc gat tat tat gag ggt aca ccg cca gat caa ggg tta Phe Asn Gly Gly Asp Tyr Tyr Glu Gly Thr Pro Pro Asp Gln Gly Leu	195	200	205	624
tct att gca cgt atg cta ggt atg ctg act tac cgc acc gat tta caa Ser Ile Ala Arg Met Leu Gly Met Leu Thr Tyr Arg Thr Asp Leu Gln	210	215	220	672
ctt gcg aaa gcc ttt ggg cgt gcc aca aaa tca gat ggc agc ttt tgg Leu Ala Lys Ala Phe Gly Arg Ala Thr Lys Ser Asp Gly Ser Phe Trp	225	230	235	240
ggc gat tac ttt caa gtg gaa tcc tat ctt tct tac caa ggc aaa aaa Gly Asp Tyr Phe Gln Val Glu Ser Tyr Leu Ser Tyr Gln Gly Lys Lys	245	250	255	768
ttc tta gaa cgt ttt gat gcc aat agt tat ttg cat ttg tta cgt gcg Phe Leu Glu Arg Phe Asp Ala Asn Ser Tyr Leu His Leu Leu Arg Ala	260	265	270	816
ttg gat atg tat gat cca agt ttg ggg tat gac aat gtt aaa gag gca Leu Asp Met Tyr Asp Pro Ser Leu Gly Tyr Asp Asn Val Lys Glu Ala	275	280	285	864

tta tca cgt att aaa gca cgc tat acg ttg gtt tct gtg aca acg gat 912
 Leu Ser Arg Ile Lys Ala Arg Tyr Thr Leu Val Ser Val Thr Thr Asp
 290 295 300

caa ctt ttt aaa ccc att gat ctt tat aaa agt aaa cag ctt tta gag 960
 Gln Leu Phe Lys Pro Ile Asp Leu Tyr Lys Ser Lys Gln Leu Leu Glu
 305 310 315 320

caa agt gga gtc gat cta cat ttt tat gaa ttc cca tca gat tac gga 1008
 Gln Ser Gly Val Asp Leu His Phe Tyr Glu Phe Pro Ser Asp Tyr Gly
 325 330 335

cac gat gcg ttt tta gtg gat tat gat cag ttt gaa aaa cga att cga 1056
 His Asp Ala Phe Leu Val Asp Tyr Asp Gln Phe Glu Lys Arg Ile Arg
 340 345 350

gat ggt ttg gca ggt aat taa 1077
 Asp Gly Leu Ala Gly Asn
 355

<210> 24
<211> 358
<212> PRT
<213> Haemophilus influenzae

<400> 24
Met Ser Val Gln Asn Val Val Leu Phe Asp Thr Gln Pro Leu Thr Leu
 1 5 10 15

Met Leu Gly Gly Lys Leu Ser His Ile Asn Val Ala Tyr Gln Thr Tyr
 20 25 30

Gly Thr Leu Asn Ala Glu Lys Asn Asn Ala Val Leu Ile Cys His Ala
 35 40 45

Leu Thr Gly Asp Ala Glu Pro Tyr Phe Asp Asp Gly Arg Asp Gly Trp
 50 55 60

Trp Gln Asn Phe Met Gly Ala Gly Leu Ala Leu Asp Thr Asp Arg Tyr
 65 70 75 80

Phe Phe Ile Ser Ser Asn Val Leu Gly Gly Cys Lys Gly Thr Thr Gly
 85 90 95

Pro Ser Ser Ile Asn Pro Gln Thr Gly Lys Pro Tyr Gly Ser Gln Phe
 100 105 110

Pro Asn Ile Val Val Gln Asp Ile Val Lys Val Gln Lys Ala Leu Leu
 115 120 125

Asp His Leu Gly Ile Ser His Leu Lys Ala Ile Ile Gly Gly Ser Phe
 130 135 140

Gly Gly Met Gln Ala Asn Gln Trp Ala Ile Asp Tyr Pro Asp Phe Met
 145 150 155 160

Asp Asn Ile Val Asn Leu Cys Ser Ser Ile Tyr Phe Ser Ala Glu Ala
 165 170 175

Ile Gly Phe Asn His Val Met Arg Gln Ala Val Ile Asn Asp Pro Asn
 180 185 190

Phe Asn Gly Gly Asp Tyr Tyr Glu Gly Thr Pro Pro Asp Gln Gly Leu
 195 200 205

Ser Ile Ala Arg Met Leu Gly Met Leu Thr Tyr Arg Thr Asp Leu Gln
 210 215 220

Leu Ala Lys Ala Phe Gly Arg Ala Thr Lys Ser Asp Gly Ser Phe Trp
 225 230 235 240

Gly Asp Tyr Phe Gln Val Glu Ser Tyr Leu Ser Tyr Gln Gly Lys Lys
 245 250 255

Phe Leu Glu Arg Phe Asp Ala Asn Ser Tyr Leu His Leu Leu Arg Ala
 260 265 270

Leu Asp Met Tyr Asp Pro Ser Leu Gly Tyr Asp Asn Val Lys Glu Ala
 275 280 285

Leu Ser Arg Ile Lys Ala Arg Tyr Thr Leu Val Ser Val Thr Thr Asp
 290 295 300

Gln Leu Phe Lys Pro Ile Asp Leu Tyr Lys Ser Lys Gln Leu Leu Glu
 305 310 315 320

Gln Ser Gly Val Asp Leu His Phe Tyr Glu Phe Pro Ser Asp Tyr Gly
 325 330 335

His Asp Ala Phe Leu Val Asp Tyr Asp Gln Phe Glu Lys Arg Ile Arg
 340 345 350

Asp Gly Leu Ala Gly Asn
 355

<210> 25
<211> 1296
<212> DNA
<213> Halobacterium sp

<220>
<221> CDS
<222> (1)..(1293)
<223> ETX_HALN1

<400> 25
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Met Gly His Asp His Gly Leu His Thr Asn Ser Val His Ala Gly Gln
 1 5 10 15

cgc gtc gac ccg gcc acg ggc gct cgc gcg ccg cca ctc tac cag acc 96
Arg Val Asp Pro Ala Thr Gly Ala Arg Ala Pro Pro Leu Tyr Gln Thr
 20 25 30

acg tcg tac gcc ttc gag gac agc gcc gat gcc gcc ggc cag ttc gcc 144
Thr Ser Tyr Ala Phe Glu Asp Ser Ala Asp Ala Ala Gly Gln Phe Ala
 35 40 45

ctt gag cgg gac ggc tac atc tac tcg cgg ctg atg aac ccc acc gtg Leu Glu Arg Asp Gly Tyr Ile Tyr Ser Arg Leu Met Asn Pro Thr Val	50	55	60	192
gag acc ctc cag gac cgc ctc gcc gcc ctc gaa ggc ggc gtc ggc gcg Glu Thr Leu Gln Asp Arg Leu Ala Ala Leu Glu Gly Gly Val Gly Ala	65	70	75	240
gtc gcc acc gcg tcc gga atg gcc ctg gac ctc gcg acg ttc ctg Val Ala Thr Ala Ser Gly Met Ala Ala Leu Asp Leu Ala Thr Phe Leu	85	90	95	288
ctg gca cgc gcc ggc gac tcc gtc gtc gcc agc gac ctc tac ggc Leu Ala Arg Ala Gly Asp Ser Val Val Ala Ala Ser Asp Leu Tyr Gly	100	105	110	336
ggc acc gtg acg tac ctc acg cac agc gcc cag cgc cgc ggc gtc gac Gly Thr Val Thr Tyr Leu Thr His Ser Ala Gln Arg Arg Gly Val Asp	115	120	125	384
acg acg ttc gtg gac gtc ctc gac tac gac gcc tac gcc gac gcc atc Thr Thr Phe Val Asp Val Leu Asp Tyr Asp Ala Tyr Ala Asp Ala Ile	130	135	140	432
gac gcc gac acc gcc tac gtg ctc gtc gaa acc gtc ggc aac ccc agc Asp Ala Asp Thr Ala Tyr Val Leu Val Glu Thr Val Gly Asn Pro Ser	145	150	155	480
145			160	
ctg atc acg ccc gac ctc gaa cgc atc gcc gac atc gcc cac gac aac Leu Ile Thr Pro Asp Leu Glu Arg Ile Ala Asp Ile Ala His Asp Asn	165	170	175	528
ggc gtt ccc ctg ctg gtg gac aac acg ttc gcg acc ccc gcg ctg gca Gly Val Pro Leu Leu Val Asp Asn Thr Phe Ala Thr Pro Ala Leu Ala	180	185	190	576
acc ccg atc gac cac ggt gcc gac atc gtc tgg cac tcc acc acc aaa Thr Pro Ile Asp His Gly Ala Asp Ile Val Trp His Ser Thr Thr Lys	195	200	205	624
tgg atc cac ggt gcc ggc acc acc gtc ggc ggc ggc ctc gtc gac gcc Trp Ile His Gly Ala Gly Thr Thr Val Gly Gly Ala Leu Val Asp Ala	210	215	220	672
ggc agc ttc gac tgg gac gcc cac gcc gac tac ccc gag atc gcc Gly Ser Phe Asp Trp Asp Ala His Ala Ala Asp Tyr Pro Glu Ile Ala	225	230	235	720
225			240	
cag gaa aac ccc gcc tac cac ggc gtg acc ttc acc gat cgc ttc ggg Gln Glu Asn Pro Ala Tyr His Gly Val Thr Phe Thr Asp Arg Phe Gly	245	250	255	768
gac gcc gcg ttc acg tac gcc gca atc gcc cgc ggg ctg cgc gat ctg Asp Ala Ala Phe Thr Tyr Ala Ala Ile Ala Arg Gly Leu Arg Asp Leu	260	265	270	816
ggc aac cag cag tcg ccg ttc gac gcc tgg cag acc ctc cag aag ctc Gly Asn Gln Gln Ser Pro Phe Asp Ala Trp Gln Thr Leu Gln Lys Leu	275	280	285	864

gaa acg ctc ccg ctg cgc atg caa caa cac tgc cg ^g aac gcc cag ctc		912
Glu Thr Leu Pro Leu Arg Met Gln Gln His Cys Arg Asn Ala Gln Leu		
290	295	300
gtc gcc gaa cac ctc cgg gac cac ccc aac gtg tcg tgg gtc aac tac		960
Val Ala Glu His Leu Arg Asp His Pro Asn Val Ser Trp Val Asn Tyr		
305	310	315
320		
ccc ggg ctg gcc gac cac gac acc cac gac aac gca acc acc tac ctc		1008
Pro Gly Leu Ala Asp His Asp Thr His Asp Asn Ala Thr Thr Tyr Leu		
325	330	335
gat tcg ggc tac gga ggc atg ctc acg ttc ggc gtc gag gac ggc tac		1056
Asp Ser Gly Tyr Gly Met Leu Thr Phe Gly Val Glu Asp Gly Tyr		
340	345	350
gag gcc gca aca tcg gtc acc gag gag acc acg ctt gcc agc ctg ctg		1104
Glu Ala Ala Gln Ser Val Thr Glu Glu Thr Thr Leu Ala Ser Leu Leu		
355	360	365
gcg aac gtc ggc gac gcc aaa acg ctc gtg atc cac ccc gcc tcc acc		1152
Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile His Pro Ala Ser Thr		
370	375	380
acc cac cag cag ctc acc ccc gaa gcc cag cgc gcc ggc ggt gtg cgc		1200
Thr His Gln Gln Leu Thr Pro Glu Ala Gln Arg Ala Gly Gly Val Arg		
385	390	395
400		
ccc gag atg gtg cgg gtg tcg gtc ggc atc gag gac ccc gcc gac atc		1248
Pro Glu Met Val Arg Val Ser Val Gly Ile Glu Asp Pro Ala Asp Ile		
405	410	415
gtc gcg gac ctc gaa acc gcc atc gag gcc gcg gtc ggg tcg gcg		1293
Val Ala Asp Leu Glu Thr Ala Ile Glu Ala Ala Val Gly Ser Ala		
420	425	430
tag		1296

<210> 26

<211> 431

<212> PRT

<213> Halobacterium sp

<400> 26

Met Gly His Asp His Gly Leu His Thr Asn Ser Val His Ala Gly Gln		
1	5	10
15		

Arg Val Asp Pro Ala Thr Gly Ala Arg Ala Pro Pro Leu Tyr Gln Thr		
20	25	30

Thr Ser Tyr Ala Phe Glu Asp Ser Ala Asp Ala Ala Gly Gln Phe Ala		
35	40	45

Leu Glu Arg Asp Gly Tyr Ile Tyr Ser Arg Leu Met Asn Pro Thr Val		
50	55	60

Glu Thr Leu Gln Asp Arg Leu Ala Ala Leu Glu Gly Gly Val Gly Ala		
65	70	75
80		

Val Ala Thr Ala Ser Gly Met Ala Ala Leu Asp Leu Ala Thr Phe Leu
 85 90 95

Leu Ala Arg Ala Gly Asp Ser Val Val Ala Ala Ser Asp Leu Tyr Gly
 100 105 110

Gly Thr Val Thr Tyr Leu Thr His Ser Ala Gln Arg Arg Gly Val Asp
 115 120 125

Thr Thr Phe Val Asp Val Leu Asp Tyr Asp Ala Tyr Ala Asp Ala Ile
 130 135 140

Asp Ala Asp Thr Ala Tyr Val Leu Val Glu Thr Val Gly Asn Pro Ser
 145 150 155 160

Leu Ile Thr Pro Asp Leu Glu Arg Ile Ala Asp Ile Ala His Asp Asn
 165 170 175

Gly Val Pro Leu Leu Val Asp Asn Thr Phe Ala Thr Pro Ala Leu Ala
 180 185 190

Thr Pro Ile Asp His Gly Ala Asp Ile Val Trp His Ser Thr Thr Lys
 195 200 205

Trp Ile His Gly Ala Gly Thr Thr Val Gly Gly Ala Leu Val Asp Ala
 210 215 220

Gly Ser Phe Asp Trp Asp Ala His Ala Ala Asp Tyr Pro Glu Ile Ala
 225 230 235 240

Gln Glu Asn Pro Ala Tyr His Gly Val Thr Phe Thr Asp Arg Phe Gly
 245 250 255

Asp Ala Ala Phe Thr Tyr Ala Ala Ile Ala Arg Gly Leu Arg Asp Leu
 • 260 265 270 •

Gly Asn Gln Gln Ser Pro Phe Asp Ala Trp Gln Thr Leu Gln Lys Leu
 275 280 285

Glu Thr Leu Pro Leu Arg Met Gln Gln His Cys Arg Asn Ala Gln Leu
 290 295 300

Val Ala Glu His Leu Arg Asp His Pro Asn Val Ser Trp Val Asn Tyr
 305 310 315 320

Pro Gly Leu Ala Asp His Asp Thr His Asp Asn Ala Thr Thr Tyr Leu
 325 330 335

Asp Ser Gly Tyr Gly Gly Met Leu Thr Phe Gly Val Glu Asp Gly Tyr
 340 345 350

Glu Ala Ala Gln Ser Val Thr Glu Glu Thr Thr Leu Ala Ser Leu Leu
 355 360 365

Ala Asn Val Gly Asp Ala Lys Thr Leu Val Ile His Pro Ala Ser Thr
 370 375 380

Thr His Gln Gln Leu Thr Pro Glu Ala Gln Arg Ala Gly Gly Val Arg
 385 390 395 400

Pro Glu Met Val Arg Val Ser Val Gly Ile Glu Asp Pro Ala Asp Ile
 405 410 415

Val Ala Asp Leu Glu Thr Ala Ile Glu Ala Ala Val Gly Ser Ala
 420 425 430

<210> 27
 <211> 1143
 <212> DNA
 <213> Thermus thermophilus

<220>
 <221> CDS
 <222> (1)..(1140)
 <223> RTT00268

<400> 27
 atg agc gag atc gcc ctc gag gcc tgg ggg gag cac gag gcc ctc ctc 48
 Met Ser Glu Ile Ala Leu Glu Ala Trp Gly Glu His Glu Ala Leu
 1 5 10 15

ctc aag ccc ccc cgc tcc ccc ctc tcc atc ccc ccg ccc aag ccc cgc 96
 Leu Lys Pro Pro Arg Ser Pro Leu Ser Ile Pro Pro Pro Lys Pro Arg
 20 25 30

acc gcc gtc ctc ttc ccc agg cgg gag ggg ttc tac acg gag ctc ggg 144
 Thr Ala Val Leu Phe Pro Arg Arg Glu Gly Phe Tyr Thr Glu Leu Gly
 35 40 45

ggg tac ctc ccc gag gtg cgc ctc cgc ttt gag acc tac ggg acc ctc 192
 Gly Tyr Leu Pro Glu Val Arg Leu Arg Phe Glu Thr Tyr Gly Thr Leu
 50 55 60

tcc cgc agg cgg gat aac gcc gtc ctc gtc ttc cac gcc ctc acg ggg 240
 Ser Arg Arg Arg Asp Asn Ala Val Leu Val Phe His Ala Leu Thr Gly
 65 70 75 80

agc gcc cac ctg gcg ggg acc tac gac gag gaa acc ttt aga agc ctc 288
 Ser Ala His Leu Ala Gly Thr Tyr Asp Glu Glu Thr Phe Arg Ser Leu
 85 90 95

tcc ccc ctg gag cag gcc ttc ggc cgg gaa ggg tgg tgg gac agc ctg 336
 Ser Pro Leu Glu Gln Ala Phe Gly Arg Glu Gly Trp Trp Asp Ser Leu
 100 105 110

gtg ggg ccc ggg cgg atc ctg gac ccc gcc ctc tac tac gtg gtc tcc 384
 Val Gly Pro Gly Arg Ile Leu Asp Pro Ala Leu Tyr Tyr Val Val Ser
 115 120 125

gcc aac cac ctg gga agc tgc tac ggc tcc acc ggc ccc ctc tcc cta 432
 Ala Asn His Leu Gly Ser Cys Tyr Gly Ser Thr Gly Pro Leu Ser Leu
 130 135 140

gac ccc cac acg ggc cgc ccc tac ggg agg gac ttc cct ccc ctt acc 480
 Asp Pro His Thr Gly Arg Pro Tyr Gly Arg Asp Phe Pro Pro Leu Thr
 145 150 155 160

atc cgc gac ctg gcc cgg gcc cag gcg agg ctt ctg gac cat ctg ggg 528
 Ile Arg Asp Leu Ala Arg Ala Gln Ala Arg Leu Leu Asp His Leu Gly

165

170

175

gtg gag aag gcc atc gtc atc ggg ggg agc ctc ggg ggg atg gtg gcc		576
Val Glu Lys Ala Ile Val Ile Gly Gly Ser Leu Gly Gly Met Val Ala		
180	185	190
ctg gag ttc gcc ctc atg tac ccg gag agg gtg aag aag ctc gtg gtc		624
Leu Glu Phe Ala Leu Met Tyr Pro Glu Arg Val Lys Lys Leu Val Val		
195	200	205
ctg gcg gcc ccc gca cg ^g cac ggc ccc tgg gcc cg ^g gcc ttc aac cac		672
Leu Ala Ala Pro Ala Arg His Gly Pro Trp Ala Arg Ala Phe Asn His		
210	215	220
ctc tcc cgc cag gcc atc ctc caa gac ccc gag tac cag aag ggc aac		720
Leu Ser Arg Gln Ala Ile Leu Gln Asp Pro Glu Tyr Gln Lys Gly Asn		
225	230	235
240		
cct gcc ccc aag ggc atg gcc ctc gcc cg ^g gga atc gcc atg atg agc		768
Pro Ala Pro Lys Gly Met Ala Leu Ala Arg Gly Ile Ala Met Met Ser		
245	250	255
tac cg ^g gcc ccc gag ggg ttt gag gcc cg ^g tgg ggc g ^g c gag ccc gag		816
Tyr Arg Ala Pro Glu Gly Phe Glu Ala Arg Trp Gly Ala Glu Pro Glu		
260	265	270
ctc ggg gaa atc cac ctg gac tac cag ggg gag aag ttc ctc cg ^g cgc		864
Leu Gly Glu Ile His Leu Asp Tyr Gln Gly Glu Lys Phe Leu Arg Arg		
275	280	285
ttc cac gcc gag agc tac ctc gtc ctc tcc cg ^g gcc atg gac aac cac		912
Phe His Ala Glu Ser Tyr Leu Val Leu Ser Arg Ala Met Asp Asn His		
290	295	300
gac gtg ggc cg ^g ggc cg ^g ggc- ^g gg ^g gtg gag gag g ^g c ctg aag cg ^g ctc		960
Asp Val Gly Arg Gly Arg Gly Val Glu Glu Ala Leu Lys Arg Leu		
305	310	315
320		
agg gcc atc ccc tcc ctc ttc gtg ggc att gac acc gac ctc ctc tac		1008
Arg Ala Ile Pro Ser Leu Phe Val Gly Ile Asp Thr Asp Leu Leu Tyr		
325	330	335
ccc gcc tgg gag gtg agg cag g ^g c g ^g c aag g ^g c g ^g c ggg g ^g c cg ^g tac		1056
Pro Ala Trp Glu Val Arg Gln Ala Ala Lys Ala Ala Gly Ala Arg Tyr		
340	345	350
cg ^g gag atc aaa agc ccc cac ggg cac gac g ^g c ttc ctc ata gag acc		1104
Arg Glu Ile Lys Ser Pro His Gly His Asp Ala Phe Leu Ile Glu Thr		
355	360	365
gac cag gtg gag gag atc ctg gac g ^g c ttc ctc ccg tag		1141
Asp Gln Val Glu Glu Ile Leu Asp Ala Phe Leu Pro		
370	375	380

<210> 28

<211> 380

<212> PRT

<213> *Thermus thermophilus*

<400> 28

Met Ser Glu Ile Ala Leu Glu Ala Trp Gly Glu His Glu Ala Leu Leu
 1 5 10 15

Leu Lys Pro Pro Arg Ser Pro Leu Ser Ile Pro Pro Pro Lys Pro Arg
 20 25 30

Thr Ala Val Leu Phe Pro Arg Arg Glu Gly Phe Tyr Thr Glu Leu Gly
 35 40 45

Gly Tyr Leu Pro Glu Val Arg Leu Arg Phe Glu Thr Tyr Gly Thr Leu
 50 55 60

Ser Arg Arg Arg Asp Asn Ala Val Leu Val Phe His Ala Leu Thr Gly
 65 70 75 80

Ser Ala His Leu Ala Gly Thr Tyr Asp Glu Glu Thr Phe Arg Ser Leu
 85 90 95

Ser Pro Leu Glu Gln Ala Phe Gly Arg Glu Gly Trp Trp Asp Ser Leu
 100 105 110

Val Gly Pro Gly Arg Ile Leu Asp Pro Ala Leu Tyr Tyr Val Val Ser
 115 120 125

Ala Asn His Leu Gly Ser Cys Tyr Gly Ser Thr Gly Pro Leu Ser Leu
 130 135 140

Asp Pro His Thr Gly Arg Pro Tyr Gly Arg Asp Phe Pro Pro Leu Thr
 145 150 155 160

Ile Arg Asp Leu Ala Arg Ala Gln Ala Arg Leu Leu Asp His Leu Gly
 165 170 175

Val Glu Lys Ala Ile Val Ile Gly Gly Ser Leu Gly Gly Met Val Ala
 180 185 190

Leu Glu Phe Ala Leu Met Tyr Pro Glu Arg Val Lys Lys Leu Val Val
 195 200 205

Leu Ala Ala Pro Ala Arg His Gly Pro Trp Ala Arg Ala Phe Asn His
 210 215 220

Leu Ser Arg Gln Ala Ile Leu Gln Asp Pro Glu Tyr Gln Lys Gly Asn
 225 230 235 240

Pro Ala Pro Lys Gly Met Ala Leu Ala Arg Gly Ile Ala Met Met Ser
 245 250 255

Tyr Arg Ala Pro Glu Gly Phe Glu Ala Arg Trp Gly Ala Glu Pro Glu
 260 265 270

Leu Gly Glu Ile His Leu Asp Tyr Gln Gly Glu Lys Phe Leu Arg Arg
 275 280 285

Phe His Ala Glu Ser Tyr Leu Val Leu Ser Arg Ala Met Asp Asn His
 290 295 300

Asp Val Gly Arg Gly Arg Gly Val Glu Glu Ala Leu Lys Arg Leu
 305 310 315 320

Arg Ala Ile Pro Ser Leu Phe Val Gly Ile Asp Thr Asp Leu Leu Tyr
 325 330 335

Pro Ala Trp Glu Val Arg Gln Ala Ala Lys Ala Ala Gly Ala Arg Tyr
 340 345 350

Arg Glu Ile Lys Ser Pro His Gly His Asp Ala Phe Leu Ile Glu Thr
 355 360 365

Asp Gln Val Glu Glu Ile Leu Asp Ala Phe Leu Pro
 370 375 380

<210> 29
<211> 1005
<212> DNA
<213> Deinococcus radiodurans

<220>
<221> CDS
<222> (1)..(1002)
<223> RDR01287

<400> 29
gtg acc gcc gtg ctc gcg ggc cac gcc tct gcc ctg ctg ctg acc gaa 48
Val Thr Ala Val Leu Ala Gly His Ala Ser Ala Leu Leu Leu Thr Glu
 1 5 10 15

gaa ccc gac tgt tcg ggg ccg cag acg gtc gtt ctc ttc cgg cgt gag 96
Glu Pro Asp Cys Ser Gly Pro Gln Thr Val Val Leu Phe Arg Arg Glu
 20 25 30

ccg ctg ctg ctc gac tgc gga ccg gcg ctg agc gac gtg cgg gtg gcc 144
Pro Leu Leu Asp Cys Gly Arg Ala Leu Ser Asp Val Arg Val Ala
 35 40 45

ttt cac acc tac ggc acg ccg cgc gcc gac gac acg ctg gtg ctg cac 192
Phe His Thr Tyr Gly Thr Pro Arg Ala Asp Ala Thr Leu Val Leu His
 50 55 60

gcc ctg acc ggc gac agc gcg gtg cac gag tgg tgg ccc gac ttt ctg 240
Ala Leu Thr Gly Asp Ser Ala Val His Glu Trp Trp Pro Asp Phe Leu
 65 70 75 80

ggc gcg ggc ccg cca ctg gac ccg gca gac gac tac gtg gtg tgc gcc 288
Gly Ala Gly Arg Pro Leu Asp Pro Ala Asp Asp Tyr Val Val Cys Ala
 85 90 95

aac gtc ctc ggc ggg tgc gcc ggc acg acg agc gac gct gaa ctc gcc 336
Asn Val Leu Gly Gly Cys Ala Gly Thr Thr Ser Ala Ala Glu Leu Ala
 100 105 110

gcc acc tgt tcc gga ccg gtg ccg ctc agc ctg cgc gac atg gcc cgg 384
Ala Thr Cys Ser Gly Pro Val Pro Leu Ser Leu Arg Asp Met Ala Arg
 115 120 125

gtg ggg cgc gcc ctg ctg gat tct ctc ggc gtg cga cgg gtg cgg gtc 432
Val Gly Arg Ala Leu Leu Asp Ser Leu Gly Val Arg Arg Val Arg Val
 130 135 140

atc ggc gcg agc atg ggc ggg atg ctc gcc tac gcc tgg ctg ctg gag		480
Ile Gly Ala Ser Met Gly Gly Met Leu Ala Tyr Ala Trp Leu Leu Glu		
145	150	155
160		
tgc ccc gac ctg gtg gaa aag gcc gtg att ata gga gcc ccg gcg cg		528
Cys Pro Asp Leu Val Glu Lys Ala Val Ile Ile Gly Ala Pro Ala Arg		
165	170	175
cac tcg ccc tgg gct att gga ctg aac acg gcg gcc cgc agc gcc att		576
His Ser Pro Trp Ala Ile Gly Leu Asn Thr Ala Ala Arg Ser Ala Ile		
180	185	190
gcc ctc gct ccc ggc ggc gag ggg ctg aag gtg gcg cgc cag att gcc		624
Ala Leu Ala Pro Gly Gly Glu Leu Lys Val Ala Arg Gln Ile Ala		
195	200	205
atg ctc agt tac cgc agc ccc gaa agc cta agc cgc acg cag gcg ggg		672
Met Leu Ser Tyr Arg Ser Pro Glu Ser Leu Ser Arg Thr Gln Ala Gly		
210	215	220
cag cgc gtg ccg ggg gtg ccc gcc gtt acg tct tac ctg cac tac caa		720
Gln Arg Val Pro Gly Val Pro Ala Val Thr Ser Tyr Leu His Tyr Gln		
225	230	235
240		
ggc gaa aaa ctc gcc gcc cgc ttc gac gag cag acc tac tgc gcc ctc		768
Gly Glu Lys Leu Ala Ala Arg Phe Asp Glu Gln Thr Tyr Cys Ala Leu		
245	250	255
acc tgg gcg atg gac gcc ttt cag ccg agc agc gcc gac ctc aaa gcg		816
Thr Trp Ala Met Asp Ala Phe Gln Pro Ser Ser Ala Asp Leu Lys Ala		
260	265	270
gtg cgc gcg ccg gta ctc gtc gtc ggc atc tcc agc gat ctg ctc tac		864
Val Arg Ala Pro Val Leu Val Val Gly Ile Ser Ser Asp Leu Leu Tyr		
275	280	285
ccc gcc gcc gag gtc cgc gcc tgc gcc gcc gag ctt ccc cac gcc gac		912
Pro Ala Ala Glu Val Arg Ala Cys Ala Ala Glu Leu Pro His Ala Asp		
290	295	300
tac tgg gaa ctg ggc agc att cac ggc cac gac gcc ttt ttg atg gac		960
Tyr Trp Glu Leu Gly Ser Ile His Gly His Asp Ala Phe Leu Met Asp		
305	310	315
320		
cca cag gac ttg ccg gag cgg gtg ggg gcg ttt ctc agg agt		1002
Pro Gln Asp Leu Pro Glu Arg Val Gly Ala Phe Leu Arg Ser		
325	330	
tga		1005

<210> 30
<211> 334
<212> PRT
<213> Deinococcus radiodurans

<400> 30
Val Thr Ala Val Leu Ala Gly His Ala Ser Ala Leu Leu Leu Thr Glu
1 5 10 15

Glu Pro Asp Cys Ser Gly Pro Gln Thr Val Val Leu Phe Arg Arg Glu
 20 25 30

Pro Leu Leu Leu Asp Cys Gly Arg Ala Leu Ser Asp Val Arg Val Ala
 35 40 45

Phe His Thr Tyr Gly Thr Pro Arg Ala Asp Ala Thr Leu Val Leu His
 50 55 60

Ala Leu Thr Gly Asp Ser Ala Val His Glu Trp Trp Pro Asp Phe Leu
 65 70 75 80

Gly Ala Gly Arg Pro Leu Asp Pro Ala Asp Asp Tyr Val Val Cys Ala
 85 90 95

Asn Val Leu Gly Gly Cys Ala Gly Thr Thr Ser Ala Ala Glu Leu Ala
 100 105 110

Ala Thr Cys Ser Gly Pro Val Pro Leu Ser Leu Arg Asp Met Ala Arg
 115 120 125

Val Gly Arg Ala Leu Leu Asp Ser Leu Gly Val Arg Arg Val Arg Val
 130 135 140

Ile Gly Ala Ser Met Gly Gly Met Leu Ala Tyr Ala Trp Leu Leu Glu
 145 150 155 160

Cys Pro Asp Leu Val Glu Lys Ala Val Ile Ile Gly Ala Pro Ala Arg
 165 170 175

His Ser Pro Trp Ala Ile Gly Leu Asn Thr Ala Ala Arg Ser Ala Ile
 180 185 190

Ala Leu Ala Pro Gly Gly Glu Gly Leu Lys Val Ala Arg Gln Ile Ala
 195 200 205

Met Leu Ser Tyr Arg Ser Pro Glu Ser Leu Ser Arg Thr Gln Ala Gly
 210 215 220

Gln Arg Val Pro Gly Val Pro Ala Val Thr Ser Tyr Leu His Tyr Gln
 225 230 235 240

Gly Glu Lys Leu Ala Ala Arg Phe Asp Glu Gln Thr Tyr Cys Ala Leu
 245 250 255

Thr Trp Ala Met Asp Ala Phe Gln Pro Ser Ser Ala Asp Leu Lys Ala
 260 265 270

Val Arg Ala Pro Val Leu Val Val Gly Ile Ser Ser Asp Leu Leu Tyr
 275 280 285

Pro Ala Ala Glu Val Arg Ala Cys Ala Ala Glu Leu Pro His Ala Asp
 290 295 300

Tyr Trp Glu Leu Gly Ser Ile His Gly His Asp Ala Phe Leu Met Asp
 305 310 315 320

Pro Gln Asp Leu Pro Glu Arg Val Gly Ala Phe Leu Arg Ser
 325 330

<210> 31
 <211> 1461
 <212> DNA
 <213> *Saccharomyces cerevisiae*

 <220>
 <221> CDS
 <222> (1)..(1458)
 <223> RSC08123

 <400> 31
 atg tcg cat act tta aaa tcg aaa acg ctc caa gag ctg gac att gag 48
 Met Ser His Thr Leu Lys Ser Lys Thr Leu Gln Glu Leu Asp Ile Glu
 1 5 10 . 15

 gag att aag gaa act aac cca ttg ctc aaa cta gtt caa ggg cag agg 96
 Glu Ile Lys Glu Thr Asn Pro Leu Leu Lys Leu Val Gln Gly Gln Arg
 20 25 30

 att gtt caa gtt ccg gaa cta gtg ctt gag tct ggc gtg gtc ata aat 144
 Ile Val Gln Val Pro Glu Leu Val Leu Glu Ser Gly Val Val Ile Asn
 35 40 45

 aat ttc cct att gct tat aag acg tgg ggt aca ctg aat gaa gct ggt 192
 Asn Phe Pro Ile Ala Tyr Lys Thr Trp Gly Thr Leu Asn Glu Ala Gly
 50 55 60

 gat aat gtt ctg gta att tgt cat gcc ttg act ggg tcc gca gat gtt 240
 Asp Asn Val Leu Val Ile Cys His Ala Leu Thr Gly Ser Ala Asp Val
 65 70 75 80

 gct gac tgg tgg ggc cct ctt ctg ggt aac gac tta gca ttc gac cca 288
 Ala Asp Trp Trp Gly Pro Leu Leu Gly Asn Asp Leu Ala Phe Asp Pro
 85 90 95

 tca agg ttt ttt atc ata tgt tta aac tct atg ggc tct cca tat ggg 336
 Ser Arg Phe Phe Ile Ile Cys Leu Asn Ser Met Gly Ser Pro Tyr Gly
 100 105 110

 tct ttt tcg cca tta acg ata aat gag gag acg ggc gtt aga tat gga 384
 Ser Phe Ser Pro Leu Thr Ile Asn Glu Glu Thr Gly Val Arg Tyr Gly
 115 120 125

 ccc gaa ttc cca tta tgt act gtg cgc gat gac gtt aga gct cac aga 432
 Pro Glu Phe Pro Leu Cys Thr Val Arg Asp Asp Val Arg Ala His Arg
 130 135 140

 att gtt ctg gat tct ctg gga gta aag tca ata gcc tgt gtt att ggt 480
 Ile Val Leu Asp Ser Leu Gly Val Lys Ser Ile Ala Cys Val Ile Gly
 145 150 155 160

 ggc tct atg ggg ggg atg ctg agt ttg gaa tgg gct gcc atg tat ggt 528
 Gly Ser Met Gly Gly Met Leu Ser Leu Glu Trp Ala Ala Met Tyr Gly
 165 170 175

 aag gaa tat gtg aag aat atg gtt gct ctg gcg aca tca gca aga cat 576
 Lys Glu Tyr Val Lys Asn Met Val Ala Leu Ala Thr Ser Ala Arg His
 180 185 190

tct gcc tgg tgc ata tcg tgg tct gag gct caa aga caa tcg att tac Ser Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr 195 200 205	624
tca gat ccc aac tac ttg gac ggg tac tat ccg gta gag gag caa cct Ser Asp Pro Asn Tyr Leu Asp Gly Tyr Tyr Pro Val Glu Glu Gln Pro 210 215 220	672
gtg gcc gga cta tcg gct gca cgt atg tct gca ttg ttg acg tac agg Val Ala Gly Leu Ser Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg 225 230 235 240	720
aca aga aac agt ttc gag aac aaa ttc tcc aga aga tct cct tca ata Thr Arg Asn Ser Phe Glu Asn Lys Phe Ser Arg Arg Ser Pro Ser Ile 245 250 255	768
gca caa caa caa aaa gct caa agg gag gag aca cgc aaa cca tct act Ala Gln Gln Lys Ala Gln Arg Glu Glu Thr Arg Lys Pro Ser Thr 260 265 270	816
gtc agc gaa cac tcc cta caa atc cac aat gat ggg tat aaa aca aaa Val Ser Glu His Ser Leu Gln Ile His Asn Asp Gly Tyr Lys Thr Lys 275 280 285	864
gcc agc act gcc atc gct ggc att tct ggg caa aaa ggt caa agc gtg Ala Ser Thr Ala Ile Ala Gly Ile Ser Gly Gln Lys Gly Gln Ser Val 290 295 300	912
gtg tcc acc gca tct tct tcg gat tca ttg aat tct tca aca tcg atg Val Ser Thr Ala Ser Ser Asp Ser Leu Asn Ser Thr Ser Met 305 310 315 320	960
act tcg gta agt tct gta acg ggt gaa gtg aag gac ata aag cct gcg Thr Ser Val Ser Val Thr Gly Glu Val Lys Asp Ile Lys Pro Ala 325 330 335	1008
cag acg tat ttt tct gca caa agt tac ttg agg tac cag ggc aca aag Gln Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Gly Thr Lys 340 345 350	1056
ttc atc aat agg ttc gac gcc aat tgt tac att gcc atc aca cgt aaa Phe Ile Asn Arg Phe Asp Ala Asn Cys Tyr Ile Ala Ile Thr Arg Lys 355 360 365	1104
ctg gat acg cac gat ttg gca aga gac aga gta gat gac atc act gag Leu Asp Thr His Asp Leu Ala Arg Asp Arg Val Asp Asp Ile Thr Glu 370 375 380	1152
gtc ctt tct acc atc caa caa cca tcc ctg atc atc ggt atc caa tct Val Leu Ser Thr Ile Gln Gln Pro Ser Leu Ile Ile Gly Ile Gln Ser 385 390 395 400	1200
gat gga ctg ttc aca tat tca gaa caa gaa ttt ttg gct gag cac ata Asp Gly Leu Phe Thr Tyr Ser Glu Gln Glu Phe Leu Ala Glu His Ile 405 410 415	1248
ccg aag tcg caa tta gaa aaa att gaa tct ccc gaa ggc cac gat gcc Pro Lys Ser Gln Leu Glu Lys Ile Glu Ser Pro Glu Gly His Asp Ala 420 425 430	1296

tcc cta ttg gag ttt aag ctg ata aac aaa ctg ata gta caa ttt tta 1344
 Phe Leu Leu Glu Phe Lys Leu Ile Asn Lys Leu Ile Val Gln Phe Leu
 435 440 445

aaa acc aac tgc aag gcc att acc gat gcc gct cca aga gct tgg gga 1392
 Lys Thr Asn Cys Lys Ala Ile Thr Asp Ala Ala Pro Arg Ala Trp Gly
 450 455 460

ggc gac gtt ggt aac gat gaa acg aag acg tct gtc ttt ggt gag gcc 1440
 Gly Asp Val Gly Asn Asp Glu Thr Lys Thr Ser Val Phe Gly Glu Ala
 465 470 475 480

gaa gaa gtt acc aac tgg tag 1461
 Glu Glu Val Thr Asn Trp
 485

<210> 32
<211> 486
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 32
Met Ser His Thr Leu Lys Ser Lys Thr Leu Gln Glu Leu Asp Ile Glu
1 5 10 15

Glu Ile Lys Glu Thr Asn Pro Leu Leu Lys Leu Val Gln Gly Gln Arg
20 25 30

Ile Val Gln Val Pro Glu Leu Val Leu Glu Ser Gly Val Val Ile Asn
35 40 45

Asn Phe Pro Ile Ala Tyr Lys Thr Trp Gly Thr Leu Asn Glu Ala Gly
50 55 60

Asp Asn Val Leu Val Ile Cys His Ala Leu Thr Gly Ser Ala Asp Val
65 70 75 80

Ala Asp Trp Trp Gly Pro Leu Leu Gly Asn Asp Leu Ala Phe Asp Pro
85 90 95

Ser Arg Phe Phe Ile Ile Cys Leu Asn Ser Met Gly Ser Pro Tyr Gly
100 105 110

Ser Phe Ser Pro Leu Thr Ile Asn Glu Glu Thr Gly Val Arg Tyr Gly
115 120 125

Pro Glu Phe Pro Leu Cys Thr Val Arg Asp Asp Val Arg Ala His Arg
130 135 140

Ile Val Leu Asp Ser Leu Gly Val Lys Ser Ile Ala Cys Val Ile Gly
145 150 155 160

Gly Ser Met Gly Gly Met Leu Ser Leu Glu Trp Ala Ala Met Tyr Gly
165 170 175

Lys Glu Tyr Val Lys Asn Met Val Ala Leu Ala Thr Ser Ala Arg His
180 185 190

Ser Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr
 195 200 205

Ser Asp Pro Asn Tyr Leu Asp Gly Tyr Tyr Pro Val Glu Glu Gln Pro
 210 215 220

Val Ala Gly Leu Ser Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg
 225 230 235 240

Thr Arg Asn Ser Phe Glu Asn Lys Phe Ser Arg Arg Ser Pro Ser Ile
 245 250 255

Ala Gln Gln Gln Lys Ala Gln Arg Glu Glu Thr Arg Lys Pro Ser Thr
 260 265 270

Val Ser Glu His Ser Leu Gln Ile His Asn Asp Gly Tyr Lys Thr Lys
 275 280 285

Ala Ser Thr Ala Ile Ala Gly Ile Ser Gly Gln Lys Gly Gln Ser Val
 290 295 300

Val Ser Thr Ala Ser Ser Ser Asp Ser Leu Asn Ser Ser Thr Ser Met
 305 310 315 320

Thr Ser Val Ser Ser Val Thr Gly Glu Val Lys Asp Ile Lys Pro Ala
 325 330 335

Gln Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Gly Thr Lys
 340 345 350

Phe Ile Asn Arg Phe Asp Ala Asn Cys Tyr Ile Ala Ile Thr Arg Lys
 355 360 365

Leu Asp Thr His Asp Leu Ala Arg Asp Arg Val Asp Asp Ile Thr Glu
 370 375 380

Val Leu Ser Thr Ile Gln Gln Pro Ser Leu Ile Ile Gly Ile Gln Ser
 385 390 395 400

Asp Gly Leu Phe Thr Tyr Ser Glu Gln Glu Phe Leu Ala Glu His Ile
 405 410 415

Pro Lys Ser Gln Leu Glu Lys Ile Glu Ser Pro Glu Gly His Asp Ala
 420 425 430

Phe Leu Leu Glu Phe Lys Leu Ile Asn Lys Leu Ile Val Gln Phe Leu
 435 440 445

Lys Thr Asn Cys Lys Ala Ile Thr Asp Ala Ala Pro Arg Ala Trp Gly
 450 455 460

Gly Asp Val Gly Asn Asp Glu Thr Lys Thr Ser Val Phe Gly Glu Ala
 465 470 475 480

Glu Glu Val Thr Asn Trp
 485

<210> 33

<211> 1470

<212> DNA

<213> Schizosaccharomyces pombe

<220>

<221> CDS

<222> (1)...(1467)

<223> RS001936

<400> 33

atg gaa tct caa tct ccg att gaa tca att gtc ttt act gac tcc tgt 48
 Met Glu Ser Gln Ser Pro Ile Glu Ser Ile Val Phe Thr Asp Ser Cys
 1 5 10 15

cat ccg tct cag caa gaa aat aaa ttt gtt cag ctt att tca gat caa 96
 His Pro Ser Gln Gln Glu Asn Lys Phe Val Gln Leu Ile Ser Asp Gln
 20 25 30

aaa att gca att gtt ccc aaa ttt acg ttg gag tgt ggc gac atc ctt 144
 Lys Ile Ala Ile Val Pro Lys Phe Thr Leu Glu Cys Gly Asp Ile Leu
 35 40 45

tac gat gtt ccc gtt gcc ttc aag act tgg ggt act ttg aat aaa gaa 192
 Tyr Asp Val Pro Val Ala Phe Lys Thr Trp Gly Thr Leu Asn Lys Glu
 50 55 60

gga aac aat tgt ctt ctt tgt cat gct tta agt ggt tct gct gat 240
 Gly Asn Asn Cys Leu Leu Cys His Ala Leu Ser Gly Ser Ala Asp
 65 70 75 80

gct gga gat tgg tgg ggt cct tta ctc ggt cct ggt cgt gcg ttt gat 288
 Ala Gly Asp Trp Trp Gly Pro Leu Leu Gly Pro Gly Arg Ala Phe Asp
 85 90 95

cca tca cat ttc ttt atc gta tgc ctt aat tct ctt ggt agc cca tac 336
 Pro Ser His Phe Phe Ile Val Cys Leu Asn Ser Leu Gly Ser Pro Tyr
 100 105 110

gga agc gcc tct cct gtt aca tgg aac gct gag act cat agt gtt tat 384
 Gly Ser Ala Ser Pro Val Thr Trp Asn Ala Glu Thr His Ser Val Tyr
 115 120 125

ggg cca gaa ttt cct tta gca acc ata cgt gat gat gta aac atc cat 432
 Gly Pro Glu Phe Pro Leu Ala Thr Ile Arg Asp Asp Val Asn Ile His
 130 135 140

aaa ctt att tta caa aga ttg ggt gta aag caa att gct atg gca gta 480
 Lys Leu Ile Leu Gln Arg Leu Gly Val Lys Gln Ile Ala Met Ala Val
 145 150 155 160

ggt ggc tcc atg ggt ggt atg ctg gtt ttg gag tgg gca ttt gat aag 528
 Gly Gly Ser Met Gly Gly Met Leu Val Leu Glu Trp Ala Phe Asp Lys
 165 170 175

gaa ttt gtg cga tca att gtt ccc att tct acc tct ctt cgt cat tcc 576
 Glu Phe Val Arg Ser Ile Val Pro Ile Ser Thr Ser Leu Arg His Ser
 180 185 190

gcg tgg tgc att agc tgg tct gaa gcg caa cgc cag agt ata tat tct 624
 Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr Ser
 195 200 205

gac cct aag ttt aat gat gga tac tac ggc ata gac gat cag cct gta		672	
Asp Pro Lys Phe Asn Asp Gly Tyr Tyr Gly Ile Asp Asp Gln Pro Val			
210	215	220	
agt ggc ctt gga gct cgt atg tct gcc ttg ttg aca tat cgc tcc		720	
Ser Gly Leu Gly Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg Ser			
225	230	235	240
aaa tgt tct ttc gaa cgt cgc ttt gcc cgt act gtt cct gat gcg tct		768	
Lys Cys Ser Phe Glu Arg Arg Phe Ala Arg Thr Val Pro Asp Ala Ser			
245	250	255	
cgt cac ccc tat cca gat cgt tta ccc act cct ctc acg ccc agt aat		816	
Arg His Pro Tyr Pro Asp Arg Leu Pro Thr Pro Leu Thr Pro Ser Asn			
260	265	270	
gca cat tgg gtc gtt cac aac gaa gga aac cgt aat cgc cgt gaa cga		864	
Ala His Trp Val Val His Asn Glu Gly Asn Arg Asn Arg Arg Glu Arg			
275	280	285	
cct tgt cga tcc aat gga tca tca cct act tct gaa agt gct tta aat		912	
Pro Cys Arg Ser Asn Gly Ser Ser Pro Thr Ser Glu Ser Ala Leu Asn			
290	295	300	
tcc ccc gcc tct tct gtc tcg tct tta cct tct tta ggt gcc tct cag		960	
Ser Pro Ala Ser Ser Val Ser Ser Leu Pro Ser Leu Gly Ala Ser Gln			
305	310	315	320
act aca gac agt tct tcc ctt aac cag agt tcg tta tta aga cgt cct		1008	
Thr Thr Asp Ser Ser Leu Asn Gln Ser Ser Leu Leu Arg Arg Pro			
325	330	335	
gct aat act tac ttc tct gcg caa tcg tat tta cgt tac caa gcg aag		1056	
Ala Asn Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Ala Lys			
340	345	350	
aag ttt gta agt cgc ttt gat gct aat tgt tac att tcg att act aaa		1104	
Lys Phe Val Ser Arg Phe Asp Ala Asn Cys Tyr Ile Ser Ile Thr Lys			
355	360	365	
aag ttg gac acc cat gat att act cgt gga cgc ggt tca gac tct cct		1152	
Lys Leu Asp Thr His Asp Ile Thr Arg Gly Arg Gly Ser Asp Ser Pro			
370	375	380	
aag gaa gtc atg aag gat ttg tct tta ccc gta ctc gta ctc ggt att		1200	
Lys Glu Val Met Lys Asp Leu Ser Leu Pro Val Leu Val Leu Gly Ile			
385	390	395	400
gaa agc gat ggt ctt ttc aca ttt gac gaa caa gtt gaa att gcc aaa		1248	
Glu Ser Asp Gly Leu Phe Thr Phe Asp Glu Gln Val Glu Ile Ala Lys			
405	410	415	
tct ttt ccc aat gct acc ttg gaa aaa att att tcg gcc gaa ggc cac		1296	
Ser Phe Pro Asn Ala Thr Leu Glu Lys Ile Ile Ser Ala Glu Gly His			
420	425	430	
gac ggt ttt ttg ctt gag ttt act caa gta aac tca cat att caa aaa		1344	
Asp Gly Phe Leu Leu Glu Phe Thr Gln Val Asn Ser His Ile Gln Lys			
435	440	445	

ttc caa aag gaa cat tta att gat atc atg tct caa act aat tcc ttt 1392
 Phe Gln Lys Glu His Leu Ile Asp Ile Met Ser Gln Thr Asn Ser Phe
 450 455 460

gag cga ctt gat tcc caa gtt aat gat acc aac cgc gaa agc gtt ttt 1440
 Glu Arg Leu Asp Ser Gln Val Asn Asp Thr Asn Arg Glu Ser Val Phe
 465 470 475 480

gga gaa atg gaa gac ata acc tcc tgg taa 1470
 Gly Glu Met Glu Asp Ile Thr Ser Trp
 485

<210> 34
 <211> 489
 <212> PRT
 <213> Schizosaccharomyces pombe

<400> 34
 Met Glu Ser Gln Ser Pro Ile Glu Ser Ile Val Phe Thr Asp Ser Cys
 1 5 10 15

His Pro Ser Gln Gln Glu Asn Lys Phe Val Gln Leu Ile Ser Asp Gln
 20 25 30

Lys Ile Ala Ile Val Pro Lys Phe Thr Leu Glu Cys Gly Asp Ile Leu
 35 40 45

Tyr Asp Val Pro Val Ala Phe Lys Thr Trp Gly Thr Leu Asn Lys Glu
 50 55 60

Gly Asn Asn Cys Leu Leu Cys His Ala Leu Ser Gly Ser Ala Asp
 65 70 75 80

Ala Gly Asp Trp Trp Gly Pro Leu Leu Gly Pro Gly Arg Ala Phe Asp
 85 90 95

Pro Ser His Phe Phe Ile Val Cys Leu Asn Ser Leu Gly Ser Pro Tyr
 100 105 110

Gly Ser Ala Ser Pro Val Thr Trp Asn Ala Glu Thr His Ser Val Tyr
 115 120 125

Gly Pro Glu Phe Pro Leu Ala Thr Ile Arg Asp Asp Val Asn Ile His
 130 135 140

Lys Leu Ile Leu Gln Arg Leu Gly Val Lys Gln Ile Ala Met Ala Val
 145 150 155 160

Gly Gly Ser Met Gly Gly Met Leu Val Leu Glu Trp Ala Phe Asp Lys
 165 170 175

Glu Phe Val Arg Ser Ile Val Pro Ile Ser Thr Ser Leu Arg His Ser
 180 185 190

Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr Ser
 195 200 205

Asp Pro Lys Phe Asn Asp Gly Tyr Tyr Gly Ile Asp Asp Gln Pro Val

210

215

220

Ser Gly Leu Gly Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg Ser
 225 230 235 240

Lys Cys Ser Phe Glu Arg Arg Phe Ala Arg Thr Val Pro Asp Ala Ser
 245 250 255

Arg His Pro Tyr Pro Asp Arg Leu Pro Thr Pro Leu Thr Pro Ser Asn
 260 265 270

Ala His Trp Val Val His Asn Glu Gly Asn Arg Asn Arg Arg Glu Arg
 275 280 285

Pro Cys Arg Ser Asn Gly Ser Ser Pro Thr Ser Glu Ser Ala Leu Asn
 290 295 300

Ser Pro Ala Ser Ser Val Ser Ser Leu Pro Ser Leu Gly Ala Ser Gln
 305 310 315 320

Thr Thr Asp Ser Ser Leu Asn Gln Ser Ser Leu Leu Arg Arg Pro
 325 330 335

Ala Asn Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Ala Lys
 340 345 350

Lys Phe Val Ser Arg Phe Asp Ala Asn Cys Tyr Ile Ser Ile Thr Lys
 355 360 365

Lys Leu Asp Thr His Asp Ile Thr Arg Gly Arg Gly Ser Asp Ser Pro
 370 375 380

Lys Glu Val Met Lys Asp Leu Ser Leu Pro Val Leu Val Leu Gly Ile
 385 390 395 400

Glu Ser Asp Gly Leu Phe Thr Phe Asp Glu Gln Val Glu Ile Ala Lys
 405 410 415

Ser Phe Pro Asn Ala Thr Leu Glu Lys Ile Ile Ser Ala Glu Gly His
 420 425 430

Asp Gly Phe Leu Leu Glu Phe Thr Gln Val Asn Ser His Ile Gln Lys
 435 440 445

Phe Gln Lys Glu His Leu Ile Asp Ile Met Ser Gln Thr Asn Ser Phe
 450 455 460

Glu Arg Leu Asp Ser Gln Val Asn Asp Thr Asn Arg Glu Ser Val Phe
 465 470 475 480

Gly Glu Met Glu Asp Ile Thr Ser Trp
 485

<210> 35

<211> 1113

<212> DNA

<213> Xylella almond

<220>

<221> CDS
<222> (1)..(1110)
<223> RXFX01562

<400> 35
 atg acc gaa ttt atc cct ccg ggc agc cta ttc cat gcg ctc tcc tct 48
 Met Thr Glu Phe Ile Pro Pro Gly Ser Leu Phe His Ala Leu Ser Ser
 1 5 10 15

 cca ttt gcg atg aag cgt ggc gga caa ctc cac cac gcc cgcc atc gct 96
 Pro Phe Ala Met Lys Arg Gly Gly Gln Leu His His Ala Arg Ile Ala
 20 25 30

 tac gaa aca tgg ggc cgc ctc aat gcc agc gcc acc aat gcc att ctg 144
 Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu
 35 40 45

 atc atg cct ggc tta tca ccc aat gca cat gcc gca cac cat gac agc 192
 Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser
 50 55 60

 aat gct gag cca ggc tgg tgg gag tca atg cta ggt cca ggc aaa ccc 240
 Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro
 65 70 75 80

 atc gac aca gac cgt tgg ttc gtg atc tgt gtc aac tca ctt ggt agc 288
 Ile Asp Thr Asp Arg Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser
 85 90 95

 tgc aaa gga tcg act ggc cct gca tcg tac aac ccc atc acg cag gcc 336
 Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala
 100 105 110

 atg tat cgt ttg gac ttt cca gca ctg tca atc gaa gac ggg gcc aac 384
 Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn
 115 120 125

 tcc gca att gaa gtg gta cat gca ctg ggc atc aag caa ctt gcc agc 432
 Ser Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser
 130 135 140

 ctg atc ggc aat tca atg ggc ggc atg acg gca ctg gcc atc ctg ctg 480
 Leu Ile Gly Asn Ser Met Gly Gly Met Thr Ala Leu Ala Ile Leu Leu
 145 150 155 160

 tta cat cca gat ata gcc cgc agc cac atc aac atc tca ggc agc gcg 528
 Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala
 165 170 175

 cag gca tta ccg ttt tcc atc gcc att cgc tcg cta caa cgc gag gcg 576
 Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala
 180 185 190

 atc cgc ctg gac ccc cat tgg agg cag gga gac tac gac gac acc cac 624
 Ile Arg Leu Asp Pro His Trp Arg Gln Gly Asp Tyr Asp Asp Thr His
 195 200 205

 tac ccg gaa tcg ggg cta cgc atc gca cgc aaa ctt ggg gtg atc acc 672
 Tyr Pro Glu Ser Gly Leu Arg Ile Ala Arg Lys Leu Gly Val Ile Thr
 210 215 220

tac cgc tcc gcg ctg gaa tgg gac ggg cgt ttt ggc cgg gta cgc ttg Tyr Arg Ser Ala Leu Glu Trp Asp Gly Arg Phe Gly Arg Val Arg Leu 225	230	235	240	720
gat tcg gac caa acc aac gac aca cca ttc gga ctg gaa ttc caa att Asp Ser Asp Gln Thr Asn Asp Thr Pro Phe Gly Leu Glu Phe Gln Ile 245	250		255	768
gaa aac tac ttg gaa agc cat gca cac cgc ttc gtg cac acc ttc gac Glu Asn Tyr Leu Glu Ser His Ala His Arg Phe Val His Thr Phe Asp 260	265	270		816
cca aac tgc tac ctg tac agc cgc tcc atg gac tgg ttc gac gtg Pro Asn Cys Tyr Leu Tyr Leu Ser Arg Ser Met Asp Trp Phe Asp Val 275	280	285		864
gcc gag tac gcc aat gga gac att ctt gcc ggg ctg gcc agg atc cga Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg 290	295	300		912
atc caa cgc gca ctc gcc atc ggt agc cat acc gac atc ctc ttt cca Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro 305	310	315	320	960
ata caa cag caa caa caa att gcc gaa ggg cta cgc cgt ggc ggt aca Ile Gln Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Thr 325	330	335		1008
cac gcc acc ttc ctg ggc ctt gac tca ccg cag ggg cat gat gcg ttc His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe 340	345	350		1056
ctt gtg gat atc gca aga ttt ggc cct cca gtg aag gaa ttt ctg gac Leu Val Asp Ile Ala Arg Phe Gly Pro Pro Val Lys Glu Phe Leu Asp 355	360	365		1104
gaa ctg tga Glu Leu 370				1113

<210> 36
<211> 370
<212> PRT
<213> Xylella almond

<400> 36				
Met Thr Glu Phe Ile Pro Pro Gly Ser Leu Phe His Ala Leu Ser Ser 1	5	10	15	
Pro Phe Ala Met Lys Arg Gly Gly Gln Leu His His Ala Arg Ile Ala 20	25	30		
Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu 35	40	45		
Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser 50	55	60		

Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro
 65 70 75 80

Ile Asp Thr Asp Arg Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser
 85 90 95

Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala
 100 105 110

Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn
 115 120 125

Ser Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser
 130 135 140

Leu Ile Gly Asn Ser Met Gly Gly Met Thr Ala Leu Ala Ile Leu Leu
 145 150 155 160

Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala
 165 170 175

Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala
 180 185 190

Ile Arg Leu Asp Pro His Trp Arg Gln Gly Asp Tyr Asp Asp Thr His
 195 200 205

Tyr Pro Glu Ser Gly Leu Arg Ile Ala Arg Lys Leu Gly Val Ile Thr
 210 215 220

Tyr Arg Ser Ala Leu Glu Trp Asp Gly Arg Phe Gly Arg Val Arg Leu
 225 230 235 240

Asp Ser Asp Gln Thr Asn Asp Thr Pro Phe Gly Leu Glu Phe Gln Ile
 • 245 250 255 •

Glu Asn Tyr Leu Glu Ser His Ala His Arg Phe Val His Thr Phe Asp
 260 265 270

Pro Asn Cys Tyr Leu Tyr Leu Ser Arg Ser Met Asp Trp Phe Asp Val
 275 280 285

Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg
 290 295 300

Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro
 305 310 315 320

Ile Gln Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Gly Thr
 325 330 335

His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe
 340 345 350

Leu Val Asp Ile Ala Arg Phe Gly Pro Pro Val Lys Glu Phe Leu Asp
 355 360 365

Glu Leu
 370

<210> 37
<211> 1113
<212> DNA
<213> *Xylella oleander*

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<220>
<221> CDS
<222> (1)..(1110)
<223> RXFY01729
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<400> 37
atg acc gaa ttt atc cct ccg ggc agc cta ttc cat gcg ctc tcc tct 48
Met Thr Glu Phe Ile Pro Pro Gly Ser Leu Phe His Ala Leu Ser Ser
          1           5           10          15

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cca ttt gcg atg aag cgt ggc gga caa ctc cac cac gcc cgcc atc gct 96
 Pro Phe Ala Met Lys Arg Gly Gly Gln Leu His His Ala Arg Ile Ala
 20 25 30

tac gaa aca tgg ggc cgc ctc aat gcc agc gcc acc aat gcc att ctg 144
Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu
35 40 45

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atc atg cct ggc tta tca ccc aat gca cat gcc gca cac cat gac agc 192
Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser
      50           55           60

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aat gct gag cca ggc tgg tgg gag tca atg cta ggt cca ggc aaa ccc 240
Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro
   65           70           75           80

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atc gac aca gac cgt tgg ttc gtg atc tgt gtc aac tca ctt ggt agc 288
Ile Asp Thr Asp Arg Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser
85 . 90 95 .

tgc aaa gga tcg act ggc cct gca tcg tac aac ccc atc acg cag gcc	336
Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala	
100 105 110	

atg tat cgt ttg gac ttt cca gca ctg tca atc gaa gac ggg gcc aac 384
Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn
115 120 125

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gcc gca att gaa gtg gta cat gca ctg ggc atc aag caa ctt gcc agc 432
Ala Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser
    130           135           140

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ctg atc ggc aat tca atg ggg ggc atg acg aca ctg gcc atc ctg ctg 480
 Leu Ile Gly Asn Ser Met Gly Gly Met Thr Thr Leu Ala Ile Leu Leu
 145 150 155 160

tta cat cca gat att gcc cgc agc cac atc aac atc tca ggc agc gcg 528
 Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala
 165 170 175

cag gca tta ccg ttt tcc atc gcc att cgc tcg cta caa cgc gag gcg 576
Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala
180 185 190

atc cgc ctg gac ccc cat tgg aag cag gga gac tac gac gac acc cac Ile Arg Leu Asp Pro His Trp Lys Gln Gly Asp Tyr Asp Asp Thr His 195 200 205	624
tac ccg gaa tcg ggg cta cgc atc gca cgc aaa ctc ggg gtg atc acc Tyr Pro Glu Ser Gly Leu Arg Ile Ala Arg Lys Leu Gly Val Ile Thr 210 215 220	672
tac cgc tcc gcg ctg gaa tgg gac ggg cgt ttt ggc cggt gta cgc ttg Tyr Arg Ser Ala Leu Glu Trp Asp Gly Arg Phe Gly Arg Val Arg Leu 225 230 235 240	720
gat tcg gac caa acc aac gac aca cca ttc gga ctg gaa ttc caa att Asp Ser Asp Gln Thr Asn Asp Thr Pro Phe Gly Leu Glu Phe Gln Ile 245 250 255	768
gaa aac tac ttg gaa agc cat gca cac cgc ttc gtg cac acc ttc gac Glu Asn Tyr Leu Glu Ser His Ala His Arg Phe Val His Thr Phe Asp 260 265 270	816
cca aac tgc tac ctg tac ctg agc cgc tcc atg gac tgg ttc gac gtg Pro Asn Cys Tyr Leu Tyr Ser Arg Ser Met Asp Trp Phe Asp Val 275 280 285	864
gcc gag tac gcc aat gga gac att ctt gcc ggg ctg gcc agg atc cga Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg 290 295 300	912
atc caa cgc gca ctt gcc atc ggt agc cat acc gac atc ctc ttt cca Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro 305 310 315 320	960
ata caa cag caa caa caa att gcc gaa ggg cta cgc cgt ggc ggt aca Ile Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Thr 325 330 335	1008
cac gcc acc ttc ctg ggc ctt gac tca ccg cag gga cat gat gcg ttc His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe 340 345 350	1056
ctt gtg gat atc gca gga ttt ggc cct cca gtg aag gaa ttt ctg ggc Leu Val Asp Ile Ala Gly Phe Gly Pro Pro Val Lys Glu Phe Leu Gly 355 360 365	1104
gaa ctg tga Glu Leu 370	1113

<210> 38
<211> 370
<212> PRT
<213> Xylella oleander

<400> 38
Met Thr Glu Phe Ile Pro Pro Gly Ser Leu Phe His Ala Leu Ser Ser
1 5 10 15
Pro Phe Ala Met Lys Arg Gly Gly Gln Leu His His Ala Arg Ile Ala
20 25 30

Tyr Glu Thr Trp Gly Arg Leu Asn Ala Ser Ala Thr Asn Ala Ile Leu
 35 40 45

Ile Met Pro Gly Leu Ser Pro Asn Ala His Ala Ala His His Asp Ser
 50 55 60 80

Asn Ala Glu Pro Gly Trp Trp Glu Ser Met Leu Gly Pro Gly Lys Pro
 65 70 75 80

Ile Asp Thr Asp Arg Trp Phe Val Ile Cys Val Asn Ser Leu Gly Ser
 85 90 95

Cys Lys Gly Ser Thr Gly Pro Ala Ser Tyr Asn Pro Ile Thr Gln Ala
 100 105 110

Met Tyr Arg Leu Asp Phe Pro Ala Leu Ser Ile Glu Asp Gly Ala Asn
 115 120 125

Ala Ala Ile Glu Val Val His Ala Leu Gly Ile Lys Gln Leu Ala Ser
 130 135 140

Leu Ile Gly Asn Ser Met Gly Gly Met Thr Thr Leu Ala Ile Leu Leu
 145 150 155 160

Leu His Pro Asp Ile Ala Arg Ser His Ile Asn Ile Ser Gly Ser Ala
 165 170 175

Gln Ala Leu Pro Phe Ser Ile Ala Ile Arg Ser Leu Gln Arg Glu Ala
 180 185 190

Ile Arg Leu Asp Pro His Trp Lys Gln Gly Asp Tyr Asp Asp Thr His
 195 200 205

Tyr Pro Glu Ser Gly Leu Arg Ile Ala Arg Lys Leu Gly Val Ile Thr
 210 215 220

Tyr Arg Ser Ala Leu Glu Trp Asp Gly Arg Phe Gly Arg Val Arg Leu
 225 230 235 240

Asp Ser Asp Gln Thr Asn Asp Thr Pro Phe Gly Leu Glu Phe Gln Ile
 245 250 255

Glu Asn Tyr Leu Glu Ser His Ala His Arg Phe Val His Thr Phe Asp
 260 265 270

Pro Asn Cys Tyr Leu Tyr Leu Ser Arg Ser Met Asp Trp Phe Asp Val
 275 280 285

Ala Glu Tyr Ala Asn Gly Asp Ile Leu Ala Gly Leu Ala Arg Ile Arg
 290 295 300

Ile Gln Arg Ala Leu Ala Ile Gly Ser His Thr Asp Ile Leu Phe Pro
 305 310 315 320

Ile Gln Gln Gln Gln Ile Ala Glu Gly Leu Arg Arg Gly Gly Thr
 325 330 335

His Ala Thr Phe Leu Gly Leu Asp Ser Pro Gln Gly His Asp Ala Phe
 340 345 350

Leu Val Asp Ile Ala Gly Phe Gly Pro Pro Val Lys Glu Phe Leu Gly
355 360 365

Glu Leu
370

<210> 39
<211> 1578
<212> DNA
<213> *Emericella nidulans*

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<220>
<221> CDS
<222> (1)..(1575)
<223> REN00010
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<400> 39
atg agt ccg ctg aac ggc gtc gct cgt tcc ttt ccg cgg ccc ttc cag 48
Met Ser Pro Leu Asn Gly Val Ala Arg Ser Phe Pro Arg Pro Phe Gln
1 5 10 15

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gcc gtg acc agg cgg cct ttt cga gtt gtc cag ccg gcc atc gcc tgt 96
Ala Val Thr Arg Arg Pro Phe Arg Val Val Gln Pro Ala Ile Ala Cys
          20           25           30

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ccg tcc aac agc cg^g tc^g tt^t aac cat tct cga tca tta cga tca acg 144
 Pro Ser Asn Ser Arg Ser Phe Asn His Ser Arg Ser Leu Arg Ser Thr
 35 40 45

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ggg tct cag tcc ccc gct cca tcc cca cgc gac tcc tcg aat ccc gcg      192
Gly Ser Gln Ser Pro Ala Pro Ser Pro Arg Asp Ser Ser Asn Pro Ala
      50           55           60

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tcc gcg cga tct ctt ggt tca ggc cct gaa ccc tcc tat acc gcc ggc 288
 Ser .Ala Arg Ser Leu Gly Ser Gly Pro Glu Pro Ser Tyr Thr Ala Gly
 85 90 95

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cac cac gaa cga ttc cat tcc gac gaa ccg ctg ctc ctt gat tgg ggc 336
His His Glu Arg Phe His Ser Asp Glu Pro Leu Leu Leu Asp Trp Gly
          100           105           110

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ggt ttg ctt cca gaa ttt gat atc gca tat gag aca tgg ggc cag ctg 384
 Gly Leu Leu Pro Glu Phe Asp Ile Ala Tyr Glu Thr Trp Gly Gln Leu
 115 . 120 . 125

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aac gag aag aag gat aat gtc att ctg ctg cat acc ggt ctg tct gca 432
Asn Glu Lys Lys Asp Asn Val Ile Leu Leu His Thr Gly Leu Ser Ala
    130          135          140

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tct	agc	cat	gcg	cac	agc	acc	gaa	gcg	aac	ccg	aag	ccc	ggc	tgg	tgg	480
Ser	Ser	His	Ala	His	Ser	Thr	Glu	Ala	Asn	Pro	Lys	Pro	Gly	Trp	Trp	
145					150					155				160		

gag aaa ttc ata ggt cct ggg aag acg cta gat acg gac aag tac ttt 528

Glu Lys Phe Ile Gly Pro Gly Lys Thr Leu Asp Thr Asp Lys Tyr Phe			
165	170	175	
gtg atc tgc acc aat gtc ctt gga ggg tgc tac ggt agc acg ggg ccc			576
Val Ile Cys Thr Asn Val Leu Gly Gly Cys Tyr Gly Ser Thr Gly Pro			
180	185	190	
tcg acg gtg gac ccg tcg gat ggg aag aag tat gct acg cggtt ccc			624
Ser Thr Val Asp Pro Ser Asp Gly Lys Lys Tyr Ala Thr Arg Phe Pro			
195	200	205	
atc ctg aca att gaa gat atg gtg cga gcg cag ttc cgc ctt ttg gac			672
Ile Leu Thr Ile Glu Asp Met Val Arg Ala Gln Phe Arg Leu Leu Asp			
210	215	220	
cat ctt ggg gtt cgaaa ctc tac .gcgc tcc gtc ggc tcc agc atg ggt			720
His Leu Gly Val Arg Lys Leu Tyr Ala Ser Val Gly Ser Ser Met Gly			
225	230	235	240
ggt atg cag agt ctt gca gcc ggt gtt ctg ttc cca gag cga gtg ggc			768
Gly Met Gln Ser Leu Ala Ala Gly Val Leu Phe Pro Glu Arg Val Gly			
245	250	255	
aag att gtg tcg att agc ggt tgt gct cga agc cat ccg tac agc att			816
Lys Ile Val Ser Ile Ser Gly Cys Ala Arg Ser His Pro Tyr Ser Ile			
260	265	270	
gct atg cgc cat acc cag cggtt atg atg gat cca aat tgg			864
Ala Met Arg His Thr Gln Arg Gln Val Leu Met Met Asp Pro Asn Trp			
275	280	285	
gct cga ggt ttc tac tac gat tcg atc cca cct cat tca ggc atg aag			912
Ala Arg Gly Phe Tyr Tyr Asp Ser Ile Pro Pro His Ser Gly Met Lys			
290	295	300	
ctc gct cgc gag att gcc acc gtc acg tac cgc agc gga cca gaa tgg			960
Leu Ala Arg Glu Ile Ala Thr Val Thr Tyr Arg Ser Gly Pro Glu Trp			
305	310	315	320
gag aaa cgc ttt ggt cgaaa cgg gct gat ccg agc aaa cag cct gcg			1008
Glu Lys Arg Phe Gly Arg Lys Arg Ala Asp Pro Ser Lys Gln Pro Ala			
325	330	335	
ctt tgc ccc gac ttt ctc atc gag acg tat ctc gac cac gcc ggt gaa			1056
Leu Cys Pro Asp Phe Leu Ile Glu Thr Tyr Leu Asp His Ala Gly Glu			
340	345	350	
aaa ttc tgc ttg gaa tac gat gcc aac agc ctg ctc tac atc tcc aag			1104
Lys Phe Cys Leu Glu Tyr Asp Ala Asn Ser Leu Leu Tyr Ile Ser Lys			
355	360	365	
gcg atg gat ctg ttt gac cta ggg ttg act cag caa ctc gcg acg aag			1152
Ala Met Asp Leu Phe Asp Leu Gly Leu Thr Gln Gln Leu Ala Thr Lys			
370	375	380	
aag cag agg gcg gag gcc cag gcg aag att agc agc gga aca aac act			1200
Lys Gln Arg Ala Glu Ala Gln Ala Lys Ile Ser Ser Gly Thr Asn Thr			
385	390	395	400
gtc aat gat gcg tcg tgc agc ctt aca ctt cct gaa cag cca tac cag			1248

Val Asn Asp Ala Ser Cys Ser Leu Thr Leu Pro Glu Gln Pro Tyr Gln			
405	410	415	
gag cag cca tct gcc tcg aca tcc gcc gag cag tct gct tcc gct tca 1296			
Glu Gln Pro Ser Ala Ser Thr Ser Ala Glu Gln Ser Ala Ser Ala Ser			
420	425	430	
gag acc ggg tcg gct ccg aac gat ctt gtt gcc ggg ctt gcg ccg ctg 1344			
Glu Thr Gly Ser Ala Pro Asn Asp Leu Val Ala Gly Leu Ala Pro Leu			
435	440	445	
aaa gac cat cag gtg ctg gta atc gga gtc gca agc gac att ctc ttc 1392			
Lys Asp His Gln Val Leu Val Ile Gly Val Ala Ser Asp Ile Leu Phe			
450	455	460	
ccg gcg tgg caa cag cgc gag atc gcg gag act ctg att caa gca ggg 1440			
Pro Ala Trp Gln Gln Arg Glu Ile Ala Glu Thr Leu Ile Gln Ala Gly			
465	470	475	480
aac aag acc gtg gag cat att gag ctg ggc aac gac gtg tct ctc ttt 1488			
Asn Lys Thr Val Glu His Ile Glu Leu Gly Asn Asp Val Ser Leu Phe			
485	490	495	
ggc cat gac aca ttc ctc ctt gat gtc aga acg tcg gag gcg cag ttc 1536			
Gly His Asp Thr Phe Leu Leu Asp Val Arg Thr Ser Glu Ala Gln Phe			
500	505	510	
gca agt tcc gta cta gtc ggc tcg cac ata att gta caa tag 1578			
Ala Ser Ser Val Leu Val Gly Ser His Ile Ile Val Gln			
515	520	525	
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<211> 525			
<212> PRT			
<213> Emericella nidulans			
<400> 40			
Met Ser Pro Leu Asn Gly Val Ala Arg Ser Phe Pro Arg Pro Phe Gln			
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Ala Val Thr Arg Arg Pro Phe Arg Val Val Gln Pro Ala Ile Ala Cys			
20	25	30	
Pro Ser Asn Ser Arg Ser Phe Asn His Ser Arg Ser Leu Arg Ser Thr			
35	40	45	
Gly Ser Gln Ser Pro Ala Pro Ser Pro Arg Asp Ser Ser Asn Pro Ala			
50	55	60	
Leu Ser Phe Pro Cys Leu Asp Ala Gln Glu Ala Lys Ser Ala Leu Leu			
65	70	75	80
Ser Ala Arg Ser Leu Gly Ser Gly Pro Glu Pro Ser Tyr Thr Ala Gly			
85	90	95	
His His Glu Arg Phe His Ser Asp Glu Pro Leu Leu Leu Asp Trp Gly			
100	105	110	
Gly Leu Leu Pro Glu Phe Asp Ile Ala Tyr Glu Thr Trp Gly Gln Leu			

115	120	125
Asn Glu Lys Lys Asp Asn Val Ile Leu Leu His Thr Gly Leu Ser Ala		
130	135	140
Ser Ser His Ala His Ser Thr Glu Ala Asn Pro Lys Pro Gly Trp Trp		
145	150	155
160		
Glu Lys Phe Ile Gly Pro Gly Lys Thr Leu Asp Thr Asp Lys Tyr Phe		
165	170	175
Val Ile Cys Thr Asn Val Leu Gly Gly Cys Tyr Gly Ser Thr Gly Pro		
180	185	190
Ser Thr Val Asp Pro Ser Asp Gly Lys Lys Tyr Ala Thr Arg Phe Pro		
195	200	205
Ile Leu Thr Ile Glu Asp Met Val Arg Ala Gln Phe Arg Leu Leu Asp		
210	215	220
His Leu Gly Val Arg Lys Leu Tyr Ala Ser Val Gly Ser Ser Met Gly		
225	230	235
240		
Gly Met Gln Ser Leu Ala Ala Gly Val Leu Phe Pro Glu Arg Val Gly		
245	250	255
Lys Ile Val Ser Ile Ser Gly Cys Ala Arg Ser His Pro Tyr Ser Ile		
260	265	270
Ala Met Arg His Thr Gln Arg Gln Val Leu Met Met Asp Pro Asn Trp		
275	280	285
Ala Arg Gly Phe Tyr Tyr Asp Ser Ile Pro Pro His Ser Gly Met Lys		
290	295	300
Leu Ala Arg Glu Ile Ala Thr Val Thr Tyr Arg Ser Gly Pro Glu Trp		
305	310	315
320		
Glu Lys Arg Phe Gly Arg Lys Arg Ala Asp Pro Ser Lys Gln Pro Ala		
325	330	335
Leu Cys Pro Asp Phe Leu Ile Glu Thr Tyr Leu Asp His Ala Gly Glu		
340	345	350
Lys Phe Cys Leu Glu Tyr Asp Ala Asn Ser Leu Leu Tyr Ile Ser Lys		
355	360	365
Ala Met Asp Leu Phe Asp Leu Gly Leu Thr Gln Gln Leu Ala Thr Lys		
370	375	380
Lys Gln Arg Ala Glu Ala Gln Ala Lys Ile Ser Ser Gly Thr Asn Thr		
385	390	395
400		
Val Asn Asp Ala Ser Cys Ser Leu Thr Leu Pro Glu Gln Pro Tyr Gln		
405	410	415
Glu Gln Pro Ser Ala Ser Thr Ser Ala Glu Gln Ser Ala Ser Ala Ser		
420	425	430
Glu Thr Gly Ser Ala Pro Asn Asp Leu Val Ala Gly Leu Ala Pro Leu		

435

440

445

Lys Asp His Gln Val Leu Val Ile Gly Val Ala Ser Asp Ile Leu Phe
 450 455 460

Pro Ala Trp Gln Gln Arg Glu Ile Ala Glu Thr Leu Ile Gln Ala Gly
 465 470 475 480

Asn Lys Thr Val Glu His Ile Glu Leu Gly Asn Asp Val Ser Leu Phe
 485 490 495

Gly His Asp Thr Phe Leu Leu Asp Val Arg Thr Ser Glu Ala Gln Phe
 500 505 510

Ala Ser Ser Val Leu Val Gly Ser His Ile Ile Val Gln
 515 520 525

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<212> DNA
<213> Mesorhizobium loti

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<223> NP_104621

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tcg agc ccg gtg ttg cgc ttc ggg gcg gac aag ccg ctc aag ctc gac 96
Ser Ser Pro Val Leu Arg Phe Gly Ala Asp Lys Pro Leu Lys Leu Asp
 20 25 30

gcc ggc acg ctt ttg tcg ccg ttc cag atc gcc tat cag acc tac ggc 144
Ala Gly Thr Leu Leu Ser Pro Phe Gln Ile Ala Tyr Gln Thr Tyr Gly
 35 40 45

acg ctg aac gat gcc cgc tcc aat gcc atc ctc gtc tgc cat gcg ctg 192
Thr Leu Asn Asp Ala Arg Ser Asn Ala Ile Leu Val Cys His Ala Leu
 50 55 60

acc ggc gac cag cat gtc gcc aac acc aat ccg gtg acc ggc aag ccg 240
Thr Gly Asp Gln His Val Ala Asn Thr Asn Pro Val Thr Gly Lys Pro
 65 70 75 80

gga tgg tgg gaa gtg ctg atc ggc ccc ggc agg atc atc gac acc aac 288
Gly Trp Trp Glu Val Leu Ile Gly Pro Gly Arg Ile Ile Asp Thr Asn
 85 90 95

cgt ttc ttc gtc atc tgc tcc aac gtc atc ggc ggt tgt ctg ggc tcc 336
Arg Phe Phe Val Ile Cys Ser Asn Val Ile Gly Gly Cys Leu Gly Ser
 100 105 110

acc ggc ccg gcc tcg acc aac ccc gcc acc ggc aag ccc tac ggg ctc 384
Thr Gly Pro Ala Ser Thr Asn Pro Ala Thr Gly Lys Pro Tyr Gly Leu
 115 120 125

gac ctg ccg gtc atc acc atc cgc gat atg gtg cgc gcg cag cag atg		432
Asp Leu Pro Val Ile Thr Ile Arg Asp Met Val Arg Ala Gln Gln Met		
130	135	140
ctg atc gat cat ttc ggc atc gag aaa ctg ttc tgc gtg ctc ggc ggc		480
Leu Ile Asp His Phe Gly Ile Glu Lys Leu Phe Cys Val Leu Gly Gly		
145	150	155
160		
tcg atg ggc gga atg cag gtg ctg gaa tgg gcg tcg agc tac ccc gag		528
Ser Met Gly Gly Met Gln Val Leu Glu Trp Ala Ser Ser Tyr Pro Glu		
165	170	175
cgc gtc ttt tcg gca ctg ccg atc gcc acc ggc gcg cgc cat tcc tcg		576
Arg Val Phe Ser Ala Leu Pro Ile Ala Thr Gly Ala Arg His Ser Ser		
180	185	190
cag aac atc gcc ttc cac gag gtc ggc cgg cag gct gtc atg gcc gat		624
Gln Asn Ile Ala Phe His Glu Val Gly Arg Gln Ala Val Met Ala Asp		
195	200	205
ccg gac tgg cac ggc ggc aaa tat ttc gaa aac ggc aaa cgc ccg gaa		672
Pro Asp Trp His Gly Gly Lys Tyr Phe Glu Asn Gly Lys Arg Pro Glu		
210	215	220
aag ggc ctg gcg gta gcg cgc atg gcc cac ata acc tat ctg tcg		720
Lys Gly Leu Ala Val Ala Arg Met Ala Ala His Ile Thr Tyr Leu Ser		
225	230	235
240		
gaa gcc gcc ctg cac cgg aaa ttc ggc cgc aat ctg cag gat cgc gag		768
Glu Ala Ala Leu His Arg Lys Phe Gly Arg Asn Leu Gln Asp Arg Glu		
245	250	255
gcg ctg acc ttc ggc ttc gac gcc gac ttc cag atc gaa agc tat ctg		816
Ala Leu Thr Phe Gly Phe Asp Ala Asp Phe Gln Ile Glu Ser Tyr Leu		
260	265	270
cgc cac caa ggc atg acc ttc gtc gac cgc ttc gac gcc aat tcc tat		864
Arg His Gln Gly Met Thr Phe Val Asp Arg Phe Asp Ala Asn Ser Tyr		
275	280	285
ctc tac atg acg cgg tcg atg gac tat ttc gac ctc gcc gcc gat cat		912
Leu Tyr Met Thr Arg Ser Met Asp Tyr Phe Asp Leu Ala Ala Asp His		
290	295	300
ggc ggg cgg ctg gcg gat gcc ttt gcc ggc acc aaa acc cgc ttc tgc		960
Gly Gly Arg Leu Ala Asp Ala Phe Ala Gly Thr Lys Thr Arg Phe Cys		
305	310	315
320		
ctg gtg tcc acc tcg gat tgg ttg ttt ccg acc gaa gag agc cgc		1008
Leu Val Ser Phe Thr Ser Asp Trp Leu Phe Pro Thr Glu Glu Ser Arg		
325	330	335
tcg atc gtg cac gcg ctc aac gcc gcc ggc tcc gtg tcc ttc gtc		1056
Ser Ile Val His Ala Leu Asn Ala Ala Gly Ala Ser Val Ser Phe Val		
340	345	350
gaa atc gag acc gac cgc ggc cac gat gcc ttc ctg ctc gac gag ccg		1104
Glu Ile Glu Thr Asp Arg Gly His Asp Ala Phe Leu Leu Asp Glu Pro		
355	360	365

gaa ctg ttc gcc gcc atc aac ggc ttc atc ggc tcc gcg qcg cgg qcg		1152	
Glu Leu Phe Ala Ala Ile Asn Gly Phe Ile Gly Ser Ala Ala Arg Ala			
370	375	380	
aga ggg cta agc gca tga		1170	
Arg Gly Leu Ser Ala			
385			
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Ala Gly Thr Leu Leu Ser Pro Phe Gln Ile Ala Tyr Gln Thr Tyr Gly			
35	40	45	
Thr Leu Asn Asp Ala Arg Ser Asn Ala Ile Leu Val Cys His Ala Leu			
50	55	60	
Thr Gly Asp Gln His Val Ala Asn Thr Asn Pro Val Thr Gly Lys Pro			
65	70	75	80
Gly Trp Trp Glu Val Leu Ile Gly Pro Gly Arg Ile Ile Asp Thr Asn			
85	90	95	
Arg Phe Phe Val Ile Cys Ser Asn Val Ile Gly Gly Cys-Leu Gly Ser			
100	105	110	
Thr Gly Pro Ala Ser Thr Asn Pro Ala Thr Gly Lys Pro Tyr Gly Leu			
115	120	125	
Asp Leu Pro Val Ile Thr Ile Arg Asp Met Val Arg Ala Gln Gln Met			
130	135	140	
Leu Ile Asp His Phe Gly Ile Glu Lys Leu Phe Cys Val Leu Gly Gly			
145	150	155	160
Ser Met Gly Gly Met Gln Val Leu Glu Trp Ala Ser Ser Tyr Pro Glu			
165	170	175	
Arg Val Phe Ser Ala Leu Pro Ile Ala Thr Gly Ala Arg His Ser Ser			
180	185	190	
Gln Asn Ile Ala Phe His Glu Val Gly Arg Gln Ala Val Met Ala Asp			
195	200	205	
Pro Asp Trp His Gly Gly Lys Tyr Phe Glu Asn Gly Lys Arg Pro Glu			
210	215	220	
Lys Gly Leu Ala Val Ala Arg Met Ala Ala His Ile Thr Tyr Leu Ser			
225	230	235	240

Glu Ala Ala Leu His Arg Lys Phe Gly Arg Asn Leu Gln Asp Arg Glu
 245 250 255

Ala Leu Thr Phe Gly Phe Asp Ala Asp Phe Gln Ile Glu Ser Tyr Leu
 260 265 270

Arg His Gln Gly Met Thr Phe Val Asp Arg Phe Asp Ala Asn Ser Tyr
 275 280 285

Leu Tyr Met Thr Arg Ser Met Asp Tyr Phe Asp Leu Ala Ala Asp His
 290 295 300

Gly Gly Arg Leu Ala Asp Ala Phe Ala Gly Thr Lys Thr Arg Phe Cys
 305 310 315 320

Leu Val Ser Phe Thr Ser Asp Trp Leu Phe Pro Thr Glu Glu Ser Arg
 325 330 335

Ser Ile Val His Ala Leu Asn Ala Ala Gly Ala Ser Val Ser Phe Val
 340 345 350

Glu Ile Glu Thr Asp Arg Gly His Asp Ala Phe Leu Leu Asp Glu Pro
 355 360 365

Glu Leu Phe Ala Ala Ile Asn Gly Phe Ile Gly Ser Ala Ala Arg Ala
 370 375 380

Arg Gly Leu Ser Ala
 385

<210> 43
 <211> 1155
 <212> DNA
 <213> acremonium crysogenum

<220>
 <221> CDS
 <222> (1)...(1152)
 <223> P39058

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aca tag cca gaa tat cgc tct tca cac tgg aat ctg gcg tca tcc ttc 96
 Thr Xaa Pro Glu Tyr Arg Ser Ser His Trp Asn Leu Ala Ser Ser Phe
 20 25 30

gcg atg tac ccg tgg cat aca aat cgt ggg gtc gca tga atg tct caa 144
 Ala Met Tyr Pro Trp His Thr Asn Arg Gly Val Ala Xaa Met Ser Gln
 35 40 45

ggg ata act gcg tca tcg tct gcc aca cct tga cga gca gcg ccc atg 192
 Gly Ile Thr Ala Ser Ser Ala Thr Pro Xaa Arg Ala Ala Pro Met
 50 55 60

tca cct cgt ggt ggc cca cac tgt ttg gcc aag gca ggg ctt tcg ata 240

Ser Pro Arg Gly Gly Pro His Cys Leu Ala Lys Ala Gly Leu Ser Ile			
65	70	75	80
cct ctc gct act tca tca tct gcc taa att atc tcg gga gcc cct ttg			288
Pro Leu Ala Thr Ser Ser Ala Xaa Ile Ile Ser Gly Ala Pro Leu			
85	90	95	
gga gtg ctg gac cat gtt cac cg ^g acc cc ^g atg cag aag gcc agc gcc			336
Gly Val Leu Asp His Val His Arg Thr Pro Met Gln Lys Ala Ser Ala			
100	105	110	
cgt acg ggg cca agt ttc ctc gca cga cga ttc gag atg atg ttc gta			384
Arg Thr Gly Pro Ser Phe Leu Ala Arg Arg Phe Glu Met Met Phe Val			
115	120	125	
t ^{tc} atc gcc agg tgc tcg aca ggt tag gcg tca ggc aaa ttg ctg cc ^g			432
Phe Ile Ala Arg Cys Ser Thr Gly Xaa Ala Ser Gly Lys Leu Leu Pro			
130	135	140	
tag tcg gcg cat cca tgg gtg gaa tgc aca ctc tgg aat ggg cct tct			480
Xaa Ser Ala His Pro Trp Val Glu Cys Thr Leu Trp Asn Gly Pro Ser			
145	150	155	160
ttg gtc cc ^g agt acg tgc gaa aga ttg tgc cca tcg cga cat cat gcc			528
Leu Val Pro Ser Thr Cys Glu Arg Leu Cys Pro Ser Arg His His Ala			
165	170	175	
gtc aga gcg gct ggt gcg cag ctt ggt tcg aga cac aga ggc agt gca			576
Val Arg Ala Ala Gly Ala Gln Leu Gly Ser Arg His Arg Gly Ser Ala			
180	185	190	
tct atg atg acc cca agt acc tgg acg ggg agt acg acg tag acg acc			624
Ser Met Met Thr Pro Ser Thr Trp Thr Gly Ser Thr Thr Xaa Thr Thr			
195	200	205	
agc ctg tcc ggg ggc tcg aaa cag cgc gca aga ttg cga atc tca cgt			672
Ser Leu Ser Gly Gly Ser Lys Gln Arg Ala Arg Leu Arg Ile Ser Arg			
210	215	220	
aca aga gca aac ctg cga tgg acg agc gct tcc ata tgg ctc cag gag			720
Thr Arg Ala Asn Leu Arg Trp Thr Ser Ala Ser Ile Trp Leu Gln Glu			
225	230	235	240
tcc aag cc ^g gcc gga ata tca gca gcc agg atg cga aga agg aaa tca			768
Ser Lys Pro Ala Gly Ile Ser Ala Ala Arg Met Arg Arg Arg Lys Ser			
245	250	255	
acg gca cag aca gc ^g gca aca gcc acc gtg ctg gcc agc cca ttg aag			816
Thr Ala Gln Thr Ala Ala Thr Ala Thr Val Leu Ala Ser Pro Leu Lys			
260	265	270	
ccg tat ctt cct atc tcc ggt acc agg ccc aga agt ttg cc ^g cga gct			864
Pro Tyr Leu Pro Ile Ser Gly Thr Arg Pro Arg Ser Leu Pro Arg Ala			
275	280	285	
tcg acg cca act gct aca tcg cca tga cac tca agt tcg aca ccc acg			912
Ser Thr Pro Thr Ala Thr Ser Pro Xaa His Ser Ser Thr Pro Thr			
290	295	300	
aca tca gca gag gcc ggg cag gat caa tcc cgg agg ctc tgg caa tga			960

Thr Ser Ala Glu Ala Gly Gln Asp Gln Ser Arg Arg Leu Trp Gln Xaa				
305	310	,	315	320
tta cac aac cag cgt tga tca ttt gcg cca ggt cag acg gtc tgt act 1008				
Leu His Asn Gln Arg Xaa Ser Phe Ala Pro Gly Gln Thr Val Cys Thr				
325		330		335
cgt ttg acg agc acg ttg aga tgg ggc gca gta tcc caa aca gtc gtc 1056				
Arg Leu Thr Ser Thr Leu Arg Trp Gly Ala Val Ser Gln Thr Val Val				
340		345		350
ttt gcg tgg tgg aca cga atg agg gtc atg act tct ttg taa tgg aag 1104				
Phe Ala Trp Trp Thr Arg Met Arg Val Met Thr Ser Leu Xaa Trp Lys				
355		360		365
cgg aca agg tta atg atg ccg tca gag gat tcc tcg atc agt cat taa 1152				
Arg Thr Arg Leu Met Met Pro Ser Glu Asp Ser Ser Ile Ser His Xaa				
370		375		380
tgt				1155

<210> 44
<211> 384
<212> PRT
<213> acremonium crysogenum

<220>
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<222> 13 .. 13
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<220>
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<222> 18 .. 18
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<220>
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<222> 45 .. 45
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<220>
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<223> All occurrences of Xaa indicate any amino acid

<400> 44

Cys	Arg	Leu	Arg	Ser	Pro	Ile	Ala	Ser	Arg	Leu	Arg	Xaa	Met	Pro	Lys
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Thr	Xaa	Pro	Glu	Tyr	Arg	Ser	Ser	His	Trp	Asn	Leu	Ala	Ser	Ser	Phe
		20				25						30			

Ala	Met	Tyr	Pro	Trp	His	Thr	Asn	Arg	Gly	Val	Ala	Xaa	Met	Ser	Gln
	35				40						45				

Gly	Ile	Thr	Ala	Ser	Ser	Ala	Thr	Pro	Xaa	Arg	Ala	Ala	Pro	Met
	50				55				60					

Ser	Pro	Arg	Gly	Gly	Pro	His	Cys	Leu	Ala	Lys	Ala	Gly	Leu	Ser	Ile
65				70			75			80					

Pro	Leu	Ala	Thr	Ser	Ser	Ala	Xaa	Ile	Ile	Ser	Gly	Ala	Pro	Leu
			85				90			95				

Gly	Val	Leu	Asp	His	Val	His	Arg	Thr	Pro	Met	Gln	Lys	Ala	Ser	Ala
	100				105					110					

Arg	Thr	Gly	Pro	Ser	Phe	Leu	Ala	Arg	Arg	Phe	Glu	Met	Met	Phe	Val
	115				120				125						

Phe	Ile	Ala	Arg	Cys	Ser	Thr	Gly	Xaa	Ala	Ser	Gly	Lys	Leu	Leu	Pro
	130				135				140						

Xaa Ser Ala His Pro Trp Val Glu Cys Thr Leu Trp Asn Gly Pro Ser
 145 150 155 160
 Leu Val Pro Ser Thr Cys Glu Arg Leu Cys Pro Ser Arg His His Ala
 165 170 175
 Val Arg Ala Ala Gly Ala Gln Leu Gly Ser Arg His Arg Gly Ser Ala
 180 185 190
 Ser Met Met Thr Pro Ser Thr Trp Thr Gly Ser Thr Thr Xaa Thr Thr
 195 200 205
 Ser Leu Ser Gly Gly Ser Lys Gln Arg Ala Arg Leu Arg Ile Ser Arg
 210 215 220
 Thr Arg Ala Asn Leu Arg Trp Thr Ser Ala Ser Ile Trp Leu Gln Glu
 225 230 235 240
 Ser Lys Pro Ala Gly Ile Ser Ala Ala Arg Met Arg Arg Arg Lys Ser
 245 250 255
 Thr Ala Gln Thr Ala Ala Thr Ala Thr Val Leu Ala Ser Pro Leu Lys
 260 265 270
 Pro Tyr Leu Pro Ile Ser Gly Thr Arg Pro Arg Ser Leu Pro Arg Ala
 275 280 285
 Ser Thr Pro Thr Ala Thr Ser Pro Xaa His Ser Ser Ser Thr Pro Thr
 290 295 300
 Thr Ser Ala Glu Ala Gly Gln Asp Gln Ser Arg Arg Leu Trp Gln Xaa
 305 310 315 320
 Leu His Asn Gln Arg Xaa Ser Phe Ala Pro Gly Gln Thr Val Cys Thr
 - 325 330 -335
 Arg Leu Thr Ser Thr Leu Arg Trp Gly Ala Val Ser Gln Thr Val Val
 340 345 350
 Phe Ala Trp Trp Thr Arg Met Arg Val Met Thr Ser Leu Xaa Trp Lys
 355 360 365
 Arg Thr Arg Leu Met Met Pro Ser Glu Asp Ser Ser Ile Ser His Xaa
 370 375 380

<210> 45
 <211> 1077
 <212> DNA
 <213> *Pseudomonas putida*

<220>
 <221> CDS
 <222> (1)..(1074)
 <223> AAK49778

<400> 45

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acc tcc cg ⁹⁶ tt ²⁰ gat gaa cc ²⁵ g ²⁵ ctg gca ctg gcc tgc tgc ggc cgt tca ctg	
Thr Ser Arg Phe Asp Glu Pro Leu Ala Leu Ala Cys Gly Arg Ser Leu	
20 25 30	
gcc agt tac gaa ctg gtc tac gag acc tat ggc acc ctg aac gcc agc 144	
Ala Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Ser	
35 40 45	
gcg agc aac gcc gtg ctg atc tgc cat gcc ctg tcc ggc cac cac cat 192	
Ala Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His	
50 55 60	
gcc gct ggc tac cat gcc gcc acc gac cgc aag cc ²⁴⁰ g ⁷⁵ ggc tgg tgg gac	
Ala Ala Gly Tyr His Ala Ala Thr Asp Arg Lys Pro Gly Trp Trp Asp	
65 70 80	
agc tgc atc ggc ccc gga aaa cc ²⁸⁸ g ⁹⁰ atc gat acc aac cgc ttc ttc gtg	
Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Asn Arg Phe Phe Val	
85 90 95	
gtc agc ctg aac aac ctc ggc tgc aac ggc agc acc ggc ccc agc 336	
Val Ser Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Thr Gly Pro Ser	
100 105 110	
agt gtc aac cca gcc acc ggt aaa cc ³⁸⁴ c ¹¹⁵ tat ggc gcc gag ttc cc ¹²⁰ g ¹²⁵ tca gta	
Ser Val Asn Pro Ala Thr Gly Lys Pro Tyr Gly Ala Glu Phe Pro Val	
115 120 125	
ttg acc gtg gaa gac tgg gtg cac agc cag gca cc ⁴³² gg ¹³⁰ ctg gcc gac cgc	
Leu Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg	
130 135 140	
ctg ggc atc cag cag tgg gca gct atc gtc ggc ggt agc ctg ggt ggc 480	
Leu Gly Ile Gln Gln Trp Ala Ala Ile Val Gly Gly Ser Leu Gly Gly	
145 150 155 160	
atg cag gcg ctg caa tgg acg atg acc tac ccc gag cgc gta cgc cac 528	
Met Gln Ala Leu Gln Trp Thr Met Thr Tyr Pro Glu Arg Val Arg His	
165 170 175	
tgc gtc gac att gcc tcg gcc ccc aag ctg tcg gcg cag aac atc gcc 576	
Cys Val Asp Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala	
180 185 190	
ttc aac gag gtg gc ⁶²⁴ g ¹⁹⁵ cgt cag gcc att ctt acc gac cct gag tac cgc	
Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Glu Tyr Arg	
195 200 205	
aga ggc tcg ttt cca gga cca ggt gtg atc ccc aag cgc ggc ctg atg 672	
Arg Gly Ser Phe Pro Gly Pro Gly Val Ile Pro Lys Arg Gly Leu Met	
210 215 220	
ctg gca cg ⁷²⁰ atg gtc ggc cac att acc tat ctg tcc gat gat tcg atg	
Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met	
225 230 235 240	

ggt gaa aaa ttc ggc cga gag ctg aaa gcg aca agc tca act acg act		768	
Gly Glu Lys Phe Gly Arg Glu Leu Lys Ala Thr Ser Ser Thr Thr Thr			
245	250	255	
tcc aca gcg tcg agt tcc agg tcg aaa gct acc tgc gct atc agg gcg		816	
Ser Thr Ala Ser Ser Arg Ser Lys Ala Thr Cys Ala Ile Arg Ala			
260	265	270	
agg agt ttt ccg gcc gtt tcg acg cca aca cct acc ttg atg acc aag		864	
Arg Ser Phe Pro Ala Val Ser Thr Pro Thr Pro Thr Leu Met Thr Lys			
275	280	285	
gca ctg gac tat ttc gac ccg gcc acg cac ggt ggt gat ctg gcc		912	
Ala Leu Asp Tyr Phe Asp Pro Ala Ala Thr His Gly Gly Asp Leu Ala			
290	295	300	
gcc acc ctg gcc cac gtc acg gcg gac tac tgc atc tgt cgt tca cca		960	
Ala Thr Leu Ala His Val Thr Ala Asp Tyr Cys Ile Cys Arg Ser Pro			
305	310	315	320
ccg act gcg ctt ctc tcc ggc ccg ttc gcg cga gat cgt cga cgc gct		1008	
Pro Thr Ala Leu Leu Ser Gly Pro Phe Ala Arg Asp Arg Arg Arg Ala			
325	330	335	
gat ggc cgc gcg caa gaa cgt ctg cta cct gga gat cga ttc gcc cta		1056	
Asp Gly Arg Ala Gln Glu Arg Leu Leu Pro Gly Asp Arg Phe Ala Leu			
340	345	350	
cgg gca cga tgc att tcc tga		1077	
Arg Ala Arg Cys Ile Ser			
355			

<210> 46
<211> 358
<212> PRT
<213> Pseudomonas putida

<400> 46			
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Thr Ser Arg Phe Asp Glu Pro Leu Ala Leu Ala Cys Gly Arg Ser Leu			
20	25	30	
Ala Ser Tyr Glu Leu Val Tyr Glu Thr Tyr Gly Thr Leu Asn Ala Ser			
35	40	45	
Ala Ser Asn Ala Val Leu Ile Cys His Ala Leu Ser Gly His His His			
50	55	60	
Ala Ala Gly Tyr His Ala Ala Thr Asp Arg Lys Pro Gly Trp Trp Asp			
65	70	75	80
Ser Cys Ile Gly Pro Gly Lys Pro Ile Asp Thr Asn Arg Phe Phe Val			
85	90	95	
Val Ser Leu Asn Asn Leu Gly Gly Cys Asn Gly Ser Thr Gly Pro Ser			
100	105	110	

Ser Val Asn Pro Ala Thr Gly Lys Pro Tyr Gly Ala Glu Phe Pro Val
 115 120 125
 Leu Thr Val Glu Asp Trp Val His Ser Gln Ala Arg Leu Ala Asp Arg
 130 135 140
 Leu Gly Ile Gln Gln Trp Ala Ala Ile Val Gly Gly Ser Leu Gly Gly
 145 150 155 160
 Met Gln Ala Leu Gln Trp Thr Met Thr Tyr Pro Glu Arg Val Arg His
 165 170 175
 Cys Val Asp Ile Ala Ser Ala Pro Lys Leu Ser Ala Gln Asn Ile Ala
 180 185 190
 Phe Asn Glu Val Ala Arg Gln Ala Ile Leu Thr Asp Pro Glu Tyr Arg
 195 200 205
 Arg Gly Ser Phe Pro Gly Pro Gly Val Ile Pro Lys Arg Gly Leu Met
 210 215 220
 Leu Ala Arg Met Val Gly His Ile Thr Tyr Leu Ser Asp Asp Ser Met
 225 230 235 240
 Gly Glu Lys Phe Gly Arg Glu Leu Lys Ala Thr Ser Ser Thr Thr Thr
 245 250 255
 Ser Thr Ala Ser Ser Ser Arg Ser Lys Ala Thr Cys Ala Ile Arg Ala
 260 265 270
 Arg Ser Phe Pro Ala Val Ser Thr Pro Thr Pro Thr Leu Met Thr Lys
 275 280 285
 Ala Leu Asp Tyr Phe Asp Pro Ala Ala Thr His Gly Gly Asp Leu Ala
 290 295 300
 Ala Thr Leu Ala His Val Thr Ala Asp Tyr Cys Ile Cys Arg Ser Pro
 305 310 315 320
 Pro Thr Ala Leu Leu Ser Gly Pro Phe Ala Arg Asp Arg Arg Ala
 325 330 335
 Asp Gly Arg Ala Gln Glu Arg Leu Leu Pro Gly Asp Arg Phe Ala Leu
 340 345 350
 Arg Ala Arg Cys Ile Ser
 355

<210> 47
 <211> 52
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:PCR primer

<400> 47
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<210> 48
<211> 53
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 48
tctagactcg agcggccgca gccggccttt aaattgaaga cgaaagggcc tcg 53

<210> 49
<211> 47
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 49
gagatctaga cccggggatc cgctagcggg ctgctaaagg aagcgga 47

<210> 50
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 50
gagaggcgcg ccgctagcgt gggcgaagaa etccagca 38

<210> 51
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 51
gagagggcgg ccgcgc当地 tcccgcttcg tgaa 34

<210> 52
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 52
gagagggcgg ccgctcaagt cggtaagcc acgc 34

<210> 53
<211> 140
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 53
tcgaatttaa atctcgagag gcctgacgtc gggcccgta ccacgcgtca tatgactagt 60
tcggacctag ggatatcgatc gacatcgatg ctcttctgcg ttaattaaca attgggatcc 120
tcttagaccgg ggatttaaat 140

<210> 54
<211> 140
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 54
gatcatttaa atcccgggtc tagaggatcc caattttaa ttaacgcaga agagcatcga 60
tgtcgacgt atcccttaggt ccgaactagt catatgacgc gtggtaccgg gcccgacgtc 120
aggcctctcg agatttaaat 140

<210> 55
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 55
gagagcggcc gccgatcctt tttaacccat cac 33

<210> 56
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:PCR primer

<400> 56
aggagcggcc gccatcgca ttttcttttg cg 32

<210> 57
<211> 5091
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:plasmid

<400> 57

gccgcgactg ctttcgcgaa gccttgcggc gcggaaattt cctccaccga gttcgac 60
 acccctatgc caagcttctt tcacccctaaa ttcgagagat tgattctta ccgtgaaat 120
 tcttcgcaaa aatcgcccc tgatcgccct tgcgacgtt gcgtcggtgc cgctggtgc 180
 gcttggctt accgactgta tcagcgccg ctcgattaa atctcgagag gcctgacgtc 240
 gggcccgta ccacgcgtca tatgactagt tcggacctag ggatatacgac gacatcgatg 300
 ctcttcgtcg ttaattaaca attgggatcc tctagacccg ggatttaaat cgctagcggg 360
 ctgtaaagg aagcgaaaca ctagaaaaagc cagtcgcag aaacgggtgc gacccggat 420
 gaatgtcagc tactgggcta tctggacaag gaaaaacgca agcgcaaaga gaaagcagg 480
 agcttgcaagt gggcttacat ggcgatagct agactggcg gttttatgga cagcaagcga 540
 accggaattt ccagctgggg cgccctctgg taaggttggg aagccctgc aagtaaactg 600
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 tgattgtctc tgaagctctc tagggggct cacaccatag gcagataacg ttccccaccg 5040
 gtcgcctcg taagcgcaca aggactgctc ccaaagatct tcaaagccac t 5091

<210> 58
 <211> 4323
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:plasmid

<400> 58
 tcttcagcg tatggttgtc gcctgagctg tagttgcctt catcgatgaa ctgctgtaca 60
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 ttcaaaagacg tgcgtatgc tgatacgta acttgtgcag ttgtcagtgt ttgtttgccc 180
 taatgtttac cggagaaatc agtgtagaat aaacggattt ttccgtcaga tgtaaatgtg 240
 gctgaacctg accattctt gtttggctt ttaggatag aatcatttgc atcgaatttg 300
 tcgcgtctt taaagacgcg gccagcgtt ttccagctgt caatagaagt ttgcggact 360
 ttttgataga acatgttaat cgatgtgtca tccgcattt taggatctcc ggctaattgca 420
 aagacgatgt ggtagccgtg atagttgcg acagtccgt cagcgtttt taatggccag 480
 ctgtccaaa cgtccaggcc tttgcagaa gagatattt taattgtgga cgaatcaaat 540
 tcagaaactt gatattttc attttttgc tggtcaggga ttgcagcat atcatggcgt 600
 gtaatatggg aaatgccgtt tgttccctt tatggcttt gttcgtttc ttgcacaaac 660
 gcttgagttt cgcctccgtc cagcagtgcg gtagtaaagg ttaatactgt tgcttgc 720
 gcaaacttt tgatgttcat cgttcatgtc tccctttta tgtaactgtgt tagcgtctg 780
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 gga 4323

<210> 59
 <211> 35
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR Primer

<400> 59

gagagagaga cgcgtccca g tggctgagac gcata

35

<210> 60

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR Primer

<400> 60

ctctctctgt cgacgaattc aatcttacgg cctg

34

<210> 61

<211> 5860

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:plasmid

<400> 61

cccggtacca cgcgtccca g tggctgagac gcataccgta aagccccagg aaccctgtgc

60

agaaaagaaaa cactcctctg gctaggtaga cacagttat aaaggttagag ttgagcgggt

120

aactgtcagc acgttagatcg aaaggtgcac aaaggtggcc ctggtcgtac agaaatatgg

180

cggttcctcg cttgagagtg cgaaacgcat tagaaacgtc gctgaacgga tcgttgccac

240

caaagaaggct ggaaatgatg tcgtgggtgt ctgctccgca atgggagaca ccacggatga

300

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Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
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<223> Description of the artificial sequence:PCR primer

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<213> Artificial sequence

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